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(11) Publication number : 0 674 005 A2

(12) EUROPEAN PATENT APPLICATION

(21) Application number : 95301176.4

(51) Int. Cl.⁶ : C12N 15/52, C12N 9/90,
C12P 19/12

(22) Date of filing : 23.02.95

(30) Priority : 23.02.94 JP 47940/94
23.02.94 JP 47956/94
06.04.94 JP 90705/94
06.04.94 JP 90728/94

(43) Date of publication of application :
27.09.95 Bulletin 95/39

(84) Designated Contracting States :
AT BE CH DE DK ES FR GB GR IE IT LI LU MC
NL PT SE

(71) Applicant : KABUSHIKI KAISHA
HAYASHIBARA SEIBUTSU KAGAKU
KENKYUJO
2-3, 1-chome, Shimoishii
Okayama-shi Okayama (JP)

(72) Inventor : Kubota, Michio
12-6, Arujihara-cho
Ibaraki-shi, Osaka (JP)
Inventor : Tsusaki, Keiji
472, Koshinden,
Hukuda-cho
Kurashiki-shi, Okayama (JP)
Inventor : Maruta, Kazuhiko
525-3-214, Kuwano
Okayama-shi, Okayama (JP)
Inventor : Sugimoto, Toshiyuki
695-44, Higashilune
Okayama-shi, Okayama (JP)

(74) Representative : Daniels, Jeffrey Nicholas t al
Page White & Farrer
54 Doughty Street
London WC1N 2LS (GB)

(54) Non-reducing saccharide-forming enzyme, DNA encoding it, and their preparations and uses.

(57) A DNA encoding an enzyme, which forms non-reducing saccharides having trehalose structure as an end unit from amylaceous saccharides having a degree of glucose polymerization of 3 or higher, enables an industrial-scale production of a recombinant enzyme with such enzyme activity. Non-reducing saccharides obtainable by the recombinant enzyme can be used in a variety of food products, cosmetics, pharmaceuticals and feeds because of their substantial non-reducibility, mild and high-quality sweetness, adequate viscosity, and moisture-retaining ability.

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The present invention relates to a novel DNA encoding an enzyme which forms non-reducing saccharides having trehalose structure as an end unit from reducing amylaceous saccharides having a degree of glucose polymerization of 3 or higher, and a recombinant DNA and enzyme containing the DNA as well as to a transformant. The present invention further relates to preparations and uses thereof.

5 Trehalose is a disaccharide which consists of 2 glucose molecules that are linked together with their reducing groups, and, naturally, it is present in fungi, algae, insects, etc., in an extremely small quantity. Having no reducing residue within the molecule, trehalose does not cause an unsatisfactory browning reaction even when heated in the presence of amino acids or the like, and because of this it can sweeten food products without fear of causing unsatisfiable coloration and deterioration. Trehalose, however, is far from being readily prepared in a desired amount by conventional production methods, and, actually, it has not scarcely been used for sweetening food products.

10 Conventional production methods are roughly classified into 2 groups, i.e. the one using cells of microorganisms and the other employing a multi-enzymatic system wherein enzymes are allowed to act on saccharides. The former, as disclosed in Japanese Patent Laid-Open No.154,485/75, is a method comprising growing microorganisms such as bacteria and yeasts in nutrient culture media, and collecting trehalose from the proliferated cells in the resultant cultures. The latter, as disclosed in Japanese Patent Laid-Open No.216,695/83, is a method comprising providing maltose as a substrate, allowing a multi-enzymatic system using maltose- and trehalose-phosphorylases to act on maltose, and recovering the formed trehalose from the reaction system. Although the former facilitates to grow microorganisms with a relative easiness, it requires sequential complicated steps for collecting trehalose from the microorganisms containing only 15 w/w % trehalose, on a dry solid basis (d.s.b.). While the latter enables to separate trehalose with a relative easiness, but it is theoretically difficult to increase the trehalose yield by allowing enzymes to act on substrates at a considerably-high concentration because the enzymatic reaction in itself is an equilibrium reaction of 2 different types of enzymes and the equilibrium point constantly inclines to the side of forming glucose phosphate.

25 In view of the foregoing, the present inventors energetically screened enzymes which form saccharides having trehalose structure from amylaceous saccharides, and found that microorganisms such as those of the species *Rhizobium* sp. M-11 and *Arthrobacter* sp. Q36 produce a novel enzyme which forms non-reducing saccharides having trehalose structure as an end unit from reducing amylaceous saccharides having a degree of glucose polymerization of 3 or higher. Before or after this finding, it was revealed that such a non-reducing saccharide is almost quantitatively hydrolyzed into trehalose and glucose and/or maltooligosaccharides by another enzyme produced by the same microorganisms as mentioned above. Since the combination use of the enzymes enables to form a desired amount of trehalose with a relative easiness, the aforementioned objects relating to trehalose would be completely overcome. Insufficient producibility of the novel enzyme by such a microorganism results in a drawback, i.e. a relatively-large scale culture thereof is inevitable to industrially produce trehalose and/or non-reducing saccharides having trehalose structure as an end unit.

35 Recombinant DNA technology has made a remarkable progress in recent years. At present, even an enzyme whose total amino acid sequence has not been revealed can be readily prepared in a desired amount, if a gene encoding the enzyme was once isolated and the base sequence was decoded, by preparing a recombinant DNA which contains a DNA encoding the enzyme, introducing the recombinant DNA into microorganisms or cells of plants and animals, and culturing the resultant transformants. Under the background, urgently required are to find a gene encoding the enzyme and to reveal a base sequence thereof.

40 It is an aim of the present invention to provide a DNA encoding an enzyme which forms non-reducing saccharides having trehalose structure as an end unit from reducing amylaceous saccharides having a degree of glucose polymerization of 3 or higher.

45 It is a further aim of the present invention to provide a recombinant DNA which contains the DNA and a self-replicable vector.

It is yet another aim of the present invention to provide a recombinant enzyme, which forms non-reducing saccharides having trehalose structure as an end unit from reducing amylaceous saccharides having a degree of glucose polymerization of 3 or higher, by means of recombinant DNA technology.

50 It is another aim of the present invention to provide a transformant obtainable by introducing the recombinant DNA into a suitable host.

It is a further aim of the present invention to provide a preparation of the recombinant enzyme.

It is yet another aim of the present invention to provide a method to convert reducing amylaceous saccharides by using the recombinant enzyme.

55 The present invention provides a DNA encoding an enzyme which forms non-reducing saccharides having trehalose structure as an end unit from reducing amylaceous saccharides having a degree of glucose polymerization of 3 or higher.

The present invention further provides a replicable recombinant DNA which contains a self-replicable vector.

tor and a DNA which encodes a non-reducing saccharide-forming enzyme.

The present invention further provides a recombinant enzyme which forms non-reducing saccharides having trehalose structure as an end unit from reducing amylaceous saccharides having a degree of glucose polymerization of 3 or higher.

5 The present invention further provides a transformant into which a replicable recombinant DNA containing a self-replicable vector and a DNA encoding an enzyme which forms non-reducing saccharides having trehalose structure as an end unit from reducing amylaceous saccharides having a degree of glucose polymerization of 3 or higher.

10 The present invention further provides a process for producing a recombinant enzyme, which contains a step of culturing a transformant capable of forming the recombinant enzyme, and collecting the enzyme from the resultant culture.

The present invention further provides a method for converting reducing amylaceous saccharides, which contains a step of allowing the recombinant enzyme to act on reducing amylaceous saccharides having a degree of glucose polymerization of 3 or higher to form from them non-reducing saccharides having trehalose structure as an end unit.

15 The invention will now be described in further detail, by way of example only, with reference to the accompanying drawings, in which:

FIG. 1 shows the optimum temperature of enzyme M-11.

FIG. 2 shows the optimum temperature of enzyme Q36.

20 FIG. 3 shows the optimum pH of enzyme M-11.

FIG. 4 shows the optimum pH of enzyme Q36.

FIG. 5 shows the thermal stability of enzyme M-11.

FIG. 6 shows the thermal stability of enzyme Q36.

FIG. 7 shows the pH stability of enzyme M-11.

25 FIG. 8 shows the pH stability of enzyme Q36.

FIG. 9 is a restriction map of the recombinant DNA pBMT7 according to the present invention. In the figure, a bold-lined part shows a DNA encoding enzyme M-11.

FIG. 10 is a restriction map of the recombinant DNA pBQT13 according to the present invention. In the figure, a bold-lined part shows a DNA encoding enzyme Q36.

30 The DNA according to the present invention exerts the production of the non-reducing saccharide-forming enzyme encoded by the DNA in a manner that the DNA is inserted into an appropriate self-replicable vector to form a replicable recombinant DNA, followed by introducing the recombinant DNA into a host, which is incapable of producing the enzyme but readily replicable, to form a transformant.

35 Although the recombinant DNA *per se* does not produce the enzyme, the production of the enzyme encoded by the DNA is induced by introducing the recombinant DNA into a host, which is incapable of producing the enzyme but replicable with a relative easiness, to form a transformant, and culturing the transformant to produce the enzyme.

The transformant according to the present invention produces the enzyme when cultured.

40 The recombinant enzyme according to the present invention acts on reducing amylaceous saccharides having a degree of glucose polymerization of 3 or higher to form non-reducing saccharides having trehalose structure as an end unit.

The culture of the transformant according to the present invention yields a desired amount of the enzyme with a relative easiness.

45 The conversion method according to the present invention converts reducing amylaceous saccharides having a degree of glucose polymerization of 3 or higher into non-reducing saccharides having trehalose structure as an end unit.

The present invention was made based on the finding of a novel enzyme which forms non-reducing saccharides having trehalose structure as an end unit from reducing amylaceous saccharides having a degree of glucose polymerization of 3 or higher. The enzyme can be obtained from cultures of microorganisms of the species *Rhizobium* sp. M-11 and *Arthrobacter* sp. Q36 (the enzymes from *Rhizobium* sp. M-11 and *Arthrobacter* sp. Q36 are respectively designated as "enzyme M-11" and "enzyme Q36" hereinafter), and the present inventors isolated the enzyme by the combination use of conventional purification methods using column chromatography mainly, and examined the properties and features to reveal the reality, i.e. a polypeptide having the following physicochemical properties:

55 (1) Action

Forming non-reducing saccharides having trehalose structure as an end unit from reducing saccharides having a degree of glucose polymerization of 3 or higher;

(2) Molecular weight

About 76,000-87,000 daltons on sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE);

(3) Isoelectric point

About 3.6-4.6 on isoelectrophoresis;

(4) Optimum temperature

Exhibiting an optimum temperature of around 35-40°C when incubated at pH 7.0 for 60 min;

(5) Optimum pH

Exhibiting an optimum pH of around 6.4-7.2 when incubated at 40°C for 60 min;

(6) Thermal stability

Stable up to a temperature of around 35-40°C when incubated at pH 7.0 for 60 min; and

(7) pH Stability

Stable up to a pH of around 5.5-11.0 when incubated at 25°C for 16 hours.

The experiments, which were conducted to reveal the aforesaid physicochemical properties, are explained in the below:

Experiment 1

Preparation of purified enzyme

Experiment 1-1

Preparation of enzyme derived from *Rhizobium* sp. M-11

In 500-ml Erlenmeyer flasks were placed 100 ml aliquots of a liquid culture medium (pH 7.0) containing 2.0 w/v % maltose, 0.5 w/v % peptone, 0.1 w/v % yeast extract, 0.1 w/v % disodium hydrogen phosphate, and 0.1 w/v % potassium dihydrogen phosphate, and the flasks were autoclaved at 120°C for 20 min to effect sterilization. After cooling the flasks a seed culture of *Rhizobium* sp. M-11 was inoculated into each liquid culture medium in each flask, followed by the incubation at 27°C for 24 hours under rotary-shaking conditions. Twenty L of a fresh preparation of the same liquid culture medium was put in a 30-L jar fermentor and sterilized, followed by inoculating one v/v % of the culture obtained in the above into the sterilized liquid culture medium in the jar fermentor, and incubating it at a pH of 6-8 and 30°C for 24 hours under aeration and agitation conditions.

Thereafter, about 18 L of the resultant culture was subjected to an ultra-high pressure cell disrupting apparatus to disrupt cells, and the resultant suspension was centrifuged to obtain a supernatant, and to about 16 L of which was added ammonium sulfate to give a 20 w/v % saturation, allowed to stand at 4°C for one hour, and centrifuged to remove sediment. To the resultant supernatant was added ammonium sulfate to give a 60 w/v % saturation, allowed to stand at 4°C for 24 hours, and centrifuged to collect sediment which was then dissolved in a minimum amount of 10 mM phosphate buffer (pH 7.0). The resultant solution was dialyzed against 10 mM phosphate buffer (pH 7.0) for 24 hours, and centrifuged to remove insoluble substances. The supernatant thus obtained was fed to a column packed with "DEAE-TOYOPEARL®", a product for ion-exchange chromatography commercialized by Tosoh Corporation, Tokyo, Japan, which had been previously equilibrated with 10 mM phosphate buffer (pH 7.0), followed by feeding to the column a linear gradient buffer of sodium chloride ranging from 0 M to 0.5 M in 10 mM phosphate buffer (pH 7.0). Fractions containing the objective enzyme were collected from the eluate, pooled, dialyzed for 10 hours against 50 mM phosphate buffer (pH 7.0) containing 2 M ammonium sulfate, and centrifuged to remove insoluble substances. Thereafter, the resultant supernatant was fed to a column, which had been packed with "BUTYL TOYOPEARL®", a gel for hydrophobic column chromatography commercialized by Tosoh Corporation, Tokyo, Japan, and equilibrated with 50 mM phosphate buffer (pH 7.0) containing 2 M ammonium sulfate, followed by feeding to the column a linear gradient buffer of ammonium sulfate ranging from 2 M to 0 M in 50 mM phosphate buffer (pH 7.0). Fractions containing the objective enzyme were collected from the eluate, pooled, fed to a column packed with "TOYOPEARL® HW-55", a product for gel filtration column chromatography commercialized by Tosoh Corporation, Tokyo, Japan, which had been previously equilibrated with 50 mM phosphate buffer (pH 7.0), followed by feeding to the column 50 mM phosphate buffer (pH 7.0) and collecting fractions containing the objective enzyme. The enzyme thus obtained had a specific activity of about 195 units/mg protein, and the yield was about 220 units per L of the culture.

Throughout the specification the enzyme activity is expressed by the value measured on the following assay: Place 4 ml of 50 mM phosphate buffer (pH 7.0) containing 1.25 w/v % maltopentaose in a test tube, add one ml of an enzyme solution to the tube, and incubate the resultant solution at 40°C for 60 min to effect enzymatic reaction. Thereafter, heat the resultant reaction mixture at 100°C for 10 min to suspend the enzymatic reaction. Dilute the resultant reaction mixture with distilled water by 10 times, and assay the reducing activity

on the Somogyi-Nelson's method. One unit activity of the enzyme is defined as the amount of enzyme which reduces the reducing power corresponding to one μmol maltopentaose per min under the same conditions as described above.

5 Experiment 1-2

Purification of enzyme Q36

Similarly as in Experiment 1-1, a seed culture of *Arthrobacter* sp.Q36 was cultured, and the resultant culture was treated to obtain a purified enzyme Q36 having a specific activity of about 200 units/mg protein in a yield of about 295 units per L of the culture.

Experiment 2

15 Physicochemical property of enzyme

Experiment 2-1

Action

To 50 mM phosphate buffer (pH 7.0) containing 20 w/v % of glucose, maltose, maltotriose, maltotetraose, maltopentaose, maltohexaose or maltoheptaose as a substrate was added 2 units/g substrate, d.s.b., of the purified enzyme M-11 or enzyme Q36 obtained in Experiment 1, and the mixture was enzymatically reacted at 40°C for 48 hours. The reaction mixture was desalted in usual manner, fed to "WB-T-330", a column for high-performance liquid chromatography (HPLC) commercialized by Tosoh Corporation, Tokyo, Japan, followed by feeding to the column distilled water at a flow rate of 0.5 ml/min at ambient temperature to separate saccharides contained in the reaction mixture while monitoring the saccharide concentration of the eluate with "MODEL RI-8012", a differential refractometer commercialized by Wako Pure Chemical Industries, Ltd., Tokyo, Japan. The saccharide composition of the reaction mixture was given in Table 1 or 2. In the table, the symbols "P1" to "P5" were named for the formed saccharides in the order from the smallest one to the largest one in terms of their degrees of glucose polymerization.

Table 1

Substrate	Saccharide in reaction mixture	Elution time (min)	Composition (%)
Glucose	Glucose	33.4	100.0
Maltose	Maltose	28.5	100.0
Maltotriose	P1	23.3	35.0
	+ Maltotriose	25.9	65.0
Maltotetraose	P2	21.6	85.6
	+ Maltotetraose	24.1	14.4
Maltopentaose	P3	19.7	92.7
	+ Maltopentaose	22.6	7.3
Maltohexaose	p4	18.7	93.5
	+ Maltohexaose	21.4	6.5
Maltoheptaose	P5	17.8	93.4
	+ Maltoheptaose	21.0	6.7

Table 2

Substrate	Saccharide in reaction mixture	Elution time (min)	Composition (%)
Glucose	Glucose	33.4	100.0
Maltose	Maltose	28.5	100.0
Maltotriose	P1	23.3	35.5
	+ Maltotriose	25.9	64.5
Maltotetraose	P2	21.6	85.8
	+ Maltotetraose	24.1	14.2

(Continued)

Substrate	Saccharide in reaction mixture	Elution time (min)	Composition (%)
Maltopentaose	P3	19.7	92.9
	+ Maltopentaose	22.6	7.1
Maltohexaose	P4	18.7	93.2
	+ Maltohexaose	21.4	6.7
Maltoheptaose	P5	17.8	93.1
	+ Maltoheptaose	21.0	6.9

As is evident from the results in Table 1 and 2, the enzymes M-11 and Q36 newly formed saccharides from reducing saccharides having a degree of glucose polymerization of 3 or higher such as maltotriose, maltotetraose, maltopentaose, maltohexaose and maltoheptaose, but not from those having a degree of glucose polymerization less than 3 such as glucose and maltose. In the enzymatic reaction, the newly formed saccharides were P1 to P5, and the total yield of the saccharides P2 to P5 was as high as 85 w/w % or more, d.s.b.

To separate the saccharides P1 to P5, 3 jacketed stainless steel columns, having an inner diameter of 2.0 cm and a length of one m, were packed with "XT-1016, Na⁺", a strong-acid cation exchange resin commercialized by Tokyo Organic Chemical Industries, Ltd., Tokyo, Japan, and cascaded in series. The reaction mixture containing any one of saccharides P1 to P5 was separatory applied to the columns at an inner column temperature of 55°C, followed by applying to the columns with 55°C distilled water at a flow rate of SV (space velocity) 0.13. After examining the saccharide composition of the resultant eluate, a fraction containing 97 w/w or more, d.s.b., of any one of saccharides P1 to P5 was recovered and pulverized in vacuo. No substantial reducing power was detected in the purified saccharides P1 to P5 on the Somogyi-Nelson's method.

To identify the saccharides P1 to P5, 50 mg one of which was weighed, dissolved in one ml of 50 mM acetate buffer (pH 4.5), and mixed with one unit of glucoamylase, followed by incubating the mixture at 40°C for 6 hours. High-performance liquid chromatography analysis on the resultant reaction mixture detected glucose and trehalose as shown in Tables 3 and 4. When the saccharides P1 to P5 were subjected to the action of β -amylase, the saccharides P1 and P2 were not hydrolyzed by β -amylase, but the saccharides P3, P4 and P5 were respectively hydrolyzed into one mole of maltose, P2 and one mole of maltose, and P1 and 2 moles of maltose.

Table 3

Substrate	Glucose (%)	Trehalose (%)	Molar ratio*
P1	36.2	63.8	1.07
P2	52.0	48.0	2.06
P3	61.4	38.6	3.02
P4	68.3	31.7	4.09
P5	72.9	27.1	5.11

Note: The molar ratios as indicated with the symbol "*" are values calculated as moles of glucose against one mole of trehalose.

Table 4

Substrate	Glucose (%)	Trehalose (%)	Molar ratio*
P1	36.0	64.0	1.07
P2	51.5	48.5	2.02
P3	61.6	38.4	3.05
P4	68.1	31.9	4.06
P5	72.5	27.5	5.01

Note: The molar ratios as indicated with the symbol "*" are values calculated as moles of glucose against one mole of trehalose.

The results in Tables 3 and 4 strongly show that the saccharides P1 to P5 consist of one mole of trehalose and 1 to 5 moles of glucose. From the facts that glucoamylase specifically hydrolyzes the α -1,4 and α -1,6 linkages in maltooligosaccharides and that β -amylase hydrolyzes the α -1,4 linkage in maltooligosaccharides from their end terminals by maltose units, it is estimated that the saccharides P1 to P5 have a structure consisting of glucose or maltooligosaccharide having a degree of glucose polymerization of 2 to 5, both of which have a trehalose residue at their end terminals.

The total judgement of the above results identifies the saccharides P1 to P5 as α -glucosyl trehalose, α -maltosyl trehalose, α -maltotriosyl trehalose, α -maltotetraosyl trehalose and α -maltopentaosyl trehalose respectively, and this evidences that the enzymes have an activity of forming non-reducing saccharides having trehalose structure as an end unit from reducing saccharides having a degree of glucose polymerization of 3 or higher.

Experiment 2-2Molecular weight

In accordance with the method reported by U. K. Laemmli in *Nature*, Vol.227, pp.680-685 (1970), the purified enzymes M-11 and Q36 in Experiment 1 were respectively electrophoresed on sodium dodecyl polyacrylamide gel electrophoresis to give a single protein band at a position corresponding to about 76,000-87,000 daltons. The marker proteins used in this experiment were myosin (MW=200,000 daltons), β -galactosidase (MW=116,250 daltons), phosphorylase B (MW=97,400 daltons), serum albumin (MW=66,200 daltons) and ovalbumin (MW=45,000 daltons).

Experiment 2-3Isoelectric point

The purified enzymes M-11 and Q36 obtained in Experiment 1 gave an isoelectric point of about 3.6-4.6 on isoelectrophoresis respectively.

Experiment 2-4Optimum temperature

The optimum temperature of the purified enzymes M-11 and Q36 obtained in Experiment 1 was about 35-40°C as shown in FIG. 1 or 2 when incubated in usual manner in 50 mM phosphate buffer (pH 7.0) for 60 min.

Experiment 2-5Optimum pH

The optimum pH of the purified enzymes M-11 and Q36 obtained in Experiment 1 was about 6.4-7.2 as shown in FIG. 3 or 4 when experimented in usual manner by incubating them at 40°C for 60 min in 50 mM acetate buffer, phosphate buffer or sodium carbonate-sodium hydrogen carbonate buffer having different pHs.

Experiment 2-6Thermal stability

The purified enzymes M-11 and Q36 obtained in Experiment 1 were stable up to a temperature of about 35-40°C as shown in FIGs. 5 and 6 when experimented in usual manner by incubating them in 50 mM phosphate buffer (pH 7.0) for 60 min.

Experiment 2-7pH Stability

The purified enzymes M-11 and Q36 obtained in Experiment 1 were stable up to a pH of about 5.5-11.0 as shown in FIGs. 7 and 8 when experimented in usual manner by incubating them at 25°C for 16 hours in 50 mM acetate buffer, phosphate buffer or sodium carbonate-sodium hydrogen carbonate buffer having different pHs.

Experiment 2-8Amino acid sequence containing the N-terminal

The amino acid sequence containing the N-terminal of the purified enzyme M-11 obtained in Experiment 1 was analyzed on "MODEL 470 A", a gas-phase protein sequencer commercialized by Applied Biosystems, Inc., Foster City, USA, to reveal that enzyme M-11 has an amino acid sequence as shown in SEQ ID NO:12.

The amino acid sequence containing the N-terminal of the purified enzyme Q36 was analyzed similarly

as in enzyme M-11 to reveal that it has an amino acid sequence as shown in SEQ ID NO:13.

Experiment 2-9

5 Partial amino acid sequence

An adequate amount of the purified enzyme M-11 obtained in Experiment 1-1 was weighed, dialyzed against 10 mM Tris-HCl buffer (pH 9.0) at 4°C for 18 hours, and admixed with 10 mM Tris-HCl buffer (pH 9.0) to give a concentration of about one mg/ml of the enzyme. About one ml of the resultant solution was placed
10 in a container, admixed with 10 µg lysyl endopeptidase, and incubated at 30°C for 22 hours to partially hydrolyze the enzyme. The resultant hydrolysate was applied to "CAPCELL-PAK C18", a column for reverse-phase high-performance liquid chromatography commercialized by Shiseido Co., Ltd., Tokyo, Japan, which had been previously equilibrated with 0.1 v/v % trifluoroacetate containing 16 v/v % aqueous acetonitrile, followed by feeding to the column 0.1 v/v % trifluoroacetate at a flow rate of 0.9 ml/min while increasing the concentration of
15 acetonitrile from 16 to 64 v/v % to separatory collect fractions containing a peptide fragment about 28 min or 40 min after the initiation of feeding (the peptide fragments were respectively named "peptide fragment A" and "peptide fragment B"). Fractions containing the peptide fragment A or B were separatory pooled, dried *in vacuo*, and dissolved in 0.1 v/v % trifluoroacetate containing 50 v/v % aqueous acetonitrile. Similarly as in Experiment 2-8, the peptide fragments A and B were analyzed and revealed to have an amino acid sequence
20 as shown in SEQ ID NO:14 and an amino acid sequence as shown in SEQ ID NO:15.

Similarly as in enzyme M-11, enzyme Q36 obtained in Experiment 1-2 was partially hydrolyzed, and the resultant was fed to "µBONDAPAK C18", a column for reverse-phase high-performance liquid chromatography commercialized by Japan Millipore Ltd., Tokyo, Japan, followed by feeding to the column 0.1 v/v % trifluoroacetate containing aqueous acetonitrile ranging from a concentration of 24 v/v % to 44 v/v % at a flow rate of
25 0.9 ml/min. Fractions containing a peptide fragment eluted about 22 min or about 40 min after the initiation of feeding (the fractions were respectively called "peptide fragment C" and "peptide fragment D" hereinafter) were respectively collected, pooled, dried *in vacuo*, and dissolved in 0.1 v/v % trifluoroacetate containing 50 v/v % aqueous acetonitrile. Analyses of the peptide fragments C and D conducted similarly as above revealed that they have amino acid sequences as shown in SEQ ID NOs:16 and 17, respectively.

No enzyme having these physicochemical properties has been known, and this concluded that it is a novel substance. Referring to *Rhizobium* sp. M-11, it is a microorganism which was isolated from a soil of Okayama-city, Okayama, Japan, deposited on December 24, 1992, in National Institute of Bioscience and Human-Technology Agency of Industrial Science and Technology, Tsukuba, Ibaraki, Japan, and accepted under the accession number of FERM BP-4130, and it has been maintained by the institute. *Arthrobacter* sp. Q36 is a micro-
35 organism which was isolated from a soil of Soja-city, Okayama, Japan, deposited on June 3, 1993, in the same institute, and accepted under the accession number of FERM BP-4316, and it has been maintained by the institute. Japanese Patent Application No.349,216/93 applied by the same applicant discloses the properties and features of the non-reducing saccharide-forming enzyme as well as the detailed bacteriological properties of these microorganisms.

The present inventors energetically screened a chromosomal DNA of *Rhizobium* sp. M-11 by using an oligonucleotide as a probe which had been chemically synthesized based on the partial amino acid sequence of enzyme M-11 as revealed in Experiment 2-9, and found a DNA fragment which consists of 2,316 base pairs having a base sequence as shown in the following SEQ ID NO:1 which initiates from the 5'-terminus. The decoding of the base sequence revealed that the enzyme consists of 772 amino acids as shown in SEQ ID NO:2.

Similarly as in enzyme M-11, a chromosomal DNA of enzyme Q36 was screened by using an oligonucleotide as a probe which had been chemically synthesized based on a partial amino acid sequence of enzyme Q36, and this yielded a DNA fragment having a base sequence consisting of 2,325 base pairs from the 5'-terminus as shown in SEQ ID NO:3. The base sequence was decoded to reveal that enzyme Q36 consists of 775 amino acids and has a partial amino acid sequence containing the N-terminal as shown in SEQ ID NO:4.

The sequential experimental steps used to reveal the base sequence and amino acid sequence as shown in SEQ ID NOs:1 to 4 are summarized as below:

- (1) The enzyme was isolated from a culture of a donor microorganism and highly purified. The purified enzyme was partially hydrolyzed with protease, and the resultant 2 different types of peptide fragments were isolated and determined their amino acid sequences;
- 55 (2) Separately, a chromosomal DNA was isolated from a donor microorganism's cell, purified and partially digested by a restriction enzyme to obtain a DNA fragment consisting of about 3,000-7,000 base pairs. The DNA fragment was ligated by DNA ligase to a plasmid vector, which had been previously cut with a restriction enzyme, to obtain a recombinant DNA;

(3) The recombinant DNA was introduced into *Escherichia coli* to obtain transformants, and from which an objectiv transformant containing a DNA encoding the enzyme was selected by the colony hybridization method using as a probe an oligonucleotide which had been chemically synthesized based on the aforesaid partial amino acid sequence; and

(4) The recombinant DNA was obtained from the transformant and annealed with a primer, followed by allowing a DNA polymerase to act on the resultant to extend the primer, and determining the base sequence of the resultant complementary chain DNA by the dideoxy chain termination method. The comparison of an amino acid sequence estimable from the determined base sequence with the aforesaid amino acid sequence confirmed that the base sequence encodes the enzyme.

As is explained in the above, the enzyme, which forms non-reducing saccharides having trehalose structure as an end unit from reducing amylaceous saccharides having a degree of glucose polymerization of 3 or higher, is an enzyme which was found as a result of the present inventors' long-term research. The enzyme has distinct physicochemical properties from those of other conventional enzymes. The present invention is to produce the enzyme by applying recombinant DNA technology. The recombinant DNA, and its preparation and uses are explained in detail with reference to examples.

The recombinant enzyme as referred to in the invention means the whole enzymes which are preparable by recombinant DNA technology and capable of forming non-reducing saccharides having trehalose structure as an end unit from reducing amylaceous saccharides having a degree of glucose polymerization of 3 or higher. Generally, the recombinant enzyme according to the present invention has a revealed amino acid sequence, and, as an example, the amino acid sequence, which initiates from the N-terminal as shown in SEQ ID NO:2 or 4, and homologous ones to it can be mentioned. Variants having amino acid sequences homologous to the one as shown in SEQ ID NO:2 or 4 can be obtained by replacing one or more bases in SEQ ID NO:2 or 4 with other bases without substantially alternating the inherent action of the enzyme. Although even when used the same DNA and it also depends on hosts into which the DNA is introduced, ingredients and components of nutrient culture media for culturing transformants, and their cultivation temperature and pH, there may be produced modified enzymes which have amino acid sequences similar to that of SEQ ID NO:2 or 4 as well as having an enzymatic action of the enzyme encoded by the DNA but defecting one or more amino acids located nearness to the N-terminal of the amino acid sequence as shown in SEQ ID NO:2 or 4 and/or having one or more amino acids newly added after the DNA expression to the N-terminal by the modification of intracellular enzymes of hosts. The recombinant enzyme can be obtained from cultures of transformants containing a specific DNA. Examples of such a transformant used in the invention can be prepared by introducing into hosts a DNA having either the base sequence which initiates from the N-terminal or a homologous base sequence to it or a complementary base sequence to them. Such a base sequence may be prepared by replacing one or more bases thereof without alternating the amino acid sequence encoded thereby by using degeneracy of genetic code. Needless to say, one or more bases in the base sequence, which encodes the enzyme or their variants, can be readily replaced with other bases to allow the DNA to actually express the enzyme production in hosts.

The DNA usable in the present invention includes any one of those derived from natural resources and artificially synthesized ones as long as they have such an aforementioned base sequence. The natural resources for the DNA according to the present invention are, for example, microorganisms of the genera *Rhizobium*, *Arthrobacter*, *Brevibacterium*, *Flavobacterium*, *Micrococcus*, *Curtobacterium*, *Mycobacterium* and *Terrabacter*, i.e. *Rhizobium* sp. M-11 (FERM BP-4130), *Arthrobacter* sp. Q36 (FERM BP-4316), *Brevibacterium helovolum* (ATCC 11822), *Flavobacterium aquatile* (IFO 3772), *Micrococcus luteus* (IFO 3064), *Micrococcus roseus* (ATCC 186), *Curtobacterium citreum* (IFO 15231), *Mycobacterium smegmatis* (ATCC 19420) and *Terrabacter tumescens* (IFO 12960) from which genes containing the present DNA can be obtained. The aforementioned microorganisms can be inoculated in nutrient culture media and cultured for about 1-3 days under aerobic conditions, and the resultant cells were collected from the cultures and subjected to ultrasonication or treated with a cell-wall lysis enzyme such as lysozyme or β -glucanase to extract genes containing the present DNA. In this case, a proteolytic enzyme such as protease can be used along with the cell-wall lysis enzyme, and, in the case of treating the cells with an ultrasonic disintegrator, they may be treated in the presence of a surfactant such as sodium dodecyl sulfate (SDS) or may be treated with freezing and thawing. The objective DNA is obtainable by treating the resultant with phenol extraction, alcohol sedimentation, centrifugation, protease treatment and/or ribonuclease treatment used in general in this field. To artificially synthesize the present DNA, it can be chemically synthesized by using the base sequence as shown in SEQ ID NO:1 or 3, or can be obtained in a plasmid form by inserting a DNA which encodes the amino acid sequence as shown in SEQ ID NO:2 or 4 into an appropriate self-replicable vector to obtain a recombinant DNA, introducing the recombinant DNA into an appropriate host to obtain a transformant, culturing the transformant, separating the proliferated cells from the resultant culture, and collecting plasmids containing the DNA from the cells.

Such a recombinant DNA is generally introduced into hosts in a recombinant DNA form. Generally, the recombinant DNA contains the aforesaid DNA and a self-replicable vector, and it can be prepared with a relative easiness by recombinant DNA technology in general when the material DNA is in hand. Examples of such a vector are plasmid vectors such as pBR322, pUC18, Bluescript II SK(+), pUB110, pTZ4, pC194, pHV14, TRp7, TEp7, pBS7, etc.; and phage vectors such as λ gt- λ C, λ gt- λ B, p11, ϕ 1, ϕ 105, etc. Among these plasmid- and phage-vectors, pBR322, pUC18, Bluescript II SK(+), λ gt- λ C and λ gt- λ B are satisfactorily used when the present DNA needs to be expressed in *Escherichia coli*, while pUB110, pTZ4, pC194, p11, ϕ 1 and ϕ 105 are satisfactorily used to express the DNA in microorganisms of the genus *Bacillus*. The plasmid vectors pHV14, TRp7, TEp7 and pBS7 are advantageously used when the recombinant DNA is allowed to grow in 2 or more hosts.

The methods used to insert the present DNA into such a vector in the invention may be conventional ones in general in this field. A gene containing the present DNA and a self-replicable vector are first digested by a restriction enzyme and/or ultrasonic disintegrator, then the resultant DNA fragments and vector fragments are ligated. To digest DNAs and vectors, restriction enzymes which specifically act on nucleotides, particularly, type II restriction enzymes, more particularly *Sau* 3AI, *Eco* RI, *Hind* III, *Bam* HI, *Sal* I, *Xba* I, *Sac* I, *Pst* I, etc., facilitate the ligation of the DNA fragments and vector fragments. To ligate the DNA fragments with vector fragments, they are annealed if necessary, then subjected to the action of a DNA ligase *in vivo* or *in vitro*. The recombinant DNA thus obtained is replicable without substantial limitation by introducing it into appropriate hosts, and culturing the resultant transformants.

The recombinant DNA thus obtained can be introduced into appropriate host microorganisms including *Escherichia coli* and those of the genus *Bacillus* as well as actinomyces and yeasts. In the case of using *Escherichia coli* as a host, the DNA can be introduced therein by culturing the host in the presence of the recombinant DNA and calcium ion, while in the case of using a microorganism of the genus *Bacillus* as a host the competent cell method and the colony hybridization method can be employed. Desired transformants can be cloned by the colony hybridization method or by culturing a variety of transformants in nutrient culture media containing reducing amylaceous saccharides having a degree of glucose polymerization of 3 or higher, and selecting the objective transformants which form non-reducing amylaceous saccharides having trehalose structure as an end unit from the reducing amylaceous saccharides.

The transformants thus obtained extracellularly produce the objective enzyme when cultured in nutrient culture media. Generally, liquid culture media in general supplemented with carbon sources, nitrogen sources and minerals, and, if necessary, further supplemented with small amounts of amino acids and vitamins can be used in the invention. Examples of the carbon sources are saccharides such as starch, starch hydrolysate, glucose, fructose and sucrose. Examples of the nitrogen sources are organic- and inorganic-substances containing nitrogen such as ammonia, ammonium salts, urea, nitrate, peptone, yeast extract, defatted soy bean, corn steep liquor, and beef extract. Cultures containing the objective enzyme can be prepared by inoculating the transformants into nutrient culture media, and incubating them at a temperature of 25-65°C and a pH of 2-8 for about 1-6 days under aerobic conditions by aeration and agitation. Such a culture can be used intact as an enzyme agent, and, usually, it may be disrupted prior to use with ultrasonic disintegrator and/or cell-wall lysis enzymes, followed by separating the enzyme from the intact cells and cell debris by filtration and/or centrifugation and purifying the enzyme. The methods to purify the enzyme include conventional ones in general. From cultures intact cells and cell debris are eliminated and subjected to one or more methods such as concentration, salting out, dialysis, separatory sedimentation, gel filtration chromatography, ionexchange chromatography, hydrophobic chromatography, affinity chromatography, gel electrophoresis and isoelectric point electrophoresis.

As is described above, the recombinant enzyme according to the present invention has a specific feature of forming non-reducing saccharides having trehalose structure as an end unit from reducing amylaceous saccharides having a degree of glucose polymerization of 3 or higher. The formed non-reducing saccharides have a satisfactorily mild and high-quality sweetness as well as an adequate viscosity and moisture-retaining ability, and, as a great advantageous feature, they can sweeten food products without fear of causing coloration and deterioration because they do not have a reducing residue within their molecule. By using these features a variety of amylaceous saccharides, which have been put aside because of their reducibilities, can be converted into saccharides having a satisfactory handleability and usefulness but having substantially no or extremely-reduced reducibility.

Now explaining the conversion method in more detail, reducing starch hydrolysates, which are obtainable by partially hydrolyzing amylaceous saccharides such as starch, amylopectin and amylose by acids and/or amylases, can be usually used as the substrate for the present recombinant enzyme. Such a starch hydrolysate can be obtained by conventional methods in general used in the art, and examples thereof include one or more maltooligosaccharides having a degree of glucose polymerization of 3 or higher such as maltotriose, maltotetraose, maltopentaose, maltohexaose and maltoheptaose. As described in "Handbook of Amylases and Re-

lated Enzymes", 1st edition, edited by Th Amylase Research Society of Japan, published by Pergamon Press plc, Oxford, England (1988), α -amylase, maltotetraose-forming amylase, maltopentaose-forming amylase and maltohexaose-forming amylase are especially useful to prepare the reducing amylaceous saccharides used in the invention, and, the use of any one of these amylases readily yields amylaceous saccharide mixtures rich in reducing amylaceous saccharides having a degree of glucose polymerization of 3 or higher in a considerably-high yield. If necessary, the combination use of the amylases and starch debranching enzymes such as pullulanase and isoamylase can increase the yield of the reducing amylaceous saccharides used as the substrate for the present recombinant enzyme.

In the conversion method according to the present invention, the present recombinant enzyme is allowed to coexist in an aqueous solution containing one or more of the aforesaid reducing amylaceous saccharides as a substrate, and allowing the solution to enzymatically react at a prescribed temperature and pH until a desired amount of the objective reducing amylaceous saccharides is formed. Although the enzymatic reaction proceeds even below a concentration of 0.1 w/v % of a substrate, a higher concentration of 2 w/v %, preferably, 5-50 w/v % of a substrate can be satisfactorily used to apply the present conversion method to an industrial-scale production. The temperature and pH used in the enzymatic reaction are set within the ranges of which do not inactivate the recombinant enzyme and allow the recombinant enzyme to effectively act on substrates, i.e. a temperature up to about 55°C, preferably, a temperature in the range of about 40-55°C, and a pH of 5-10, preferably, a pH in the range of about 6-8. The amount and reaction time of the present recombinant enzyme are chosen dependently on the enzymatic reaction condition. The enzymatic reaction relatively-highly reduces the reducing power of reducing amylaceous saccharides having a degree of glucose polymerization of 3 or higher, and, in the case of maltopentaose, the reducing power is lowered to about 7% against the original level.

The reaction mixtures obtained by the present conversion reaction can be used intact, and, usually, they are purified prior to use: Insoluble substances are eliminated from the reaction mixtures by filtration and centrifugation, and the resultant solutions are decolorized with an activated charcoal, desalted and purified on ion exchangers, and concentrated into syrupy products. Dependently on their use, the syrupy products are dried *in vacuo* and spray-dried into solid products. In order to obtain products which substantially consist of non-reducing saccharides, the aforesaid syrupy products are subjected to one or more methods such as chromatography using an ion exchanger, activated charcoal and silica gel for saccharide separation, separatory sedimentation using alcohol and/or acetone, membrane filtration, fermentation by yeasts, and removal and decomposition of reducing saccharides by alkalis. The methods to treat a large amount of reaction mixture are, for example, fixed bed- or pseudomoving bed-ion exchange column chromatography as disclosed in Japanese Patent Laid-Open Nos.23,799/83 and 72,598/83, and such a method produces non-reducing saccharide-rich products in an industrial scale and in a considerably-high yield.

The reducing saccharides thus obtained have a wide applicability to a variety of products which are apt to be readily damaged by the reducibility of saccharide sweeteners: For example, they can be satisfactorily used in food products, cosmetics and pharmaceuticals as a sweetener, taste-improving agent, quality-improving agent, stabilizer, filler, excipient and adjuvant. Since the non-reducing saccharides approximately qualitatively form trehalose when received an enzymatic action of a trehalose-releasing enzyme as disclosed in Japanese Patent Application No.340,343/93, they can be used as an intermediate for the production of trehalose which could not have been readily prepared.

The following examples explain the present invention in more detail, and the recombinant DNA technologies or techniques employed therein are in themselves conventional ones used in the art, for example, those described by J. Sumbruck et al. in "Molecular Cloning A Laboratory Manual", 2nd edition, published by Cold Spring Harbor Laboratory Press, USA (1989).

Example 1

Preparation of recombinant DNA containing DNA derived from enzyme M-11, and transformant

Example 1-1

Preparation of chromosomal DNA

A seed culture of *Rhizobium* sp. M-11 was inoculated into bacto nutrient broth medium (pH 7.0), and cultured at 27°C for 24 hours with a rotary shaker. The cells were separated from the resultant culture by centrifugation, suspended in TES buffer (pH 8.0), admixed with 0.05 w/v % lysozyme, and incubated at 37°C for 30 min. The resultant was freezed at -80°C for one hour, admixed with TSS buffer (pH 9.0), heated to 60°C, and admixed with a mixture solution of TES buffer and phenol, and the resultant solution was chilled with ice, fol-

lowed by centrifugally collecting the precipitated crude chromosomal DNA. To the supernatant was added 2 fold volumes of cold ethanol, and the precipitated crude chromosomal DNA was collected, suspended in SSC buffer (pH 7.1), admixed with 7.5 µg ribonuclease and 125 µg protease, and incubated at 37°C for one hour. Thereafter, a mixture solution of chloroform and isoamyl alcohol was added to the reaction mixture to extract the objective chromosomal DNA, and admixed with cold ethanol, followed by collecting the formed sediment containing the chromosomal DNA. The purified chromosomal DNA thus obtained was dissolved in SSC buffer (pH 7.1) to give a concentration of about one mg/ml, and the solution was freeze-dried at -80°C.

Example 1-2

Preparation of recombinant DNA pBMT7 and transformant BMT7

About one ml of the purified chromosomal DNA obtained in Example 1-1 was placed in a container, admixed with about 35 units of *Sau* 3AI, a restriction enzyme, and enzymatically reacted at 37°C for about 20 min to partially digest the chromosomal DNA, followed by recovering a DNA fragment consisting of about 3,000-7,000 base pairs by sucrose density-gradient ultracentrifugation. One µg of Bluescript II SK(+), a plasmid vector, was provided, subjected to the action of *Bam* HI, a restriction enzyme, to completely digest the plasmid vector, admixed with 10 µg of the DNA fragment and 2 units of T4 DNA ligase, and allowed to stand at 4°C overnight to ligate the DNA fragment to the vector fragment. To the resultant recombinant DNA was added 30 µl of "Epicurian Coli® XLI-Blue", competent cell commercialized by Toyobo Co., Ltd., Tokyo, Japan, allowed to stand under ice-chilled conditions for 30 min, heated to 42°C admixed with SOC broth, incubated at 37°C for one hour to introduce the recombinant DNA into *Escherichia coli*.

The resultant transformant was inoculated into agar plate (pH 7.0) containing 50 µg/ml of 5-bromo-4-chloro-3-indolyl-β-galactoside, and cultured at 37°C for 18 hours, followed by placing a nylon film on the agar plate to fix thereon about 4,400 colonies formed on the agar plate. Based on the amino acid sequence of Pro-Glu-Trp-Glu-Lys located at positions from 17 to 21 in the amino acid sequence of the peptide fragment A as revealed in Experiment 2-9, the base sequence of probe 1 as shown in SEQ ID NO:5 was chemically synthesized, labelled with ³²P, and hybridized with the colonies of transformants fixed on the nylon film, followed by selecting 9 transformants which exhibited a strong hybridization.

The objective recombinant DNA was selected in usual manner from the 9 transformants, and, in accordance with the method described by E. M. Southern in *Journal of Molecular Biology*, Vol.98, pp.503-517 (1975), hybridized with probe 2 having the base sequence as shown in SEQ ID NO:6 which had been chemically synthesized based on the amino acid sequence of Thr-Glu-Phe-Trp-Asp located at positions from 16 to 20 in the amino acid sequence of the peptide fragment B as revealed in Experiment 2-9, followed by selecting a recombinant DNA which strongly hybridized with probe 2. The recombinant DNA and transformant thus selected were respectively named pBMT7 and BMT7.

The transformant BMT7 obtained in the above was inoculated into L-broth (pH 7.0) containing 100 µg/ml ampicillin, and cultured at 37°C for 24 hours with a rotary shaker. After completion of the culture, the cells were collected from the culture by centrifugation, and treated with the alkaline method in general to extracellularly extract a recombinant DNA. The resultant was in usual manner purified and analyzed to find that the recombinant DNA pBMT7 consists of about 9,300 base pairs and has a structure expressed by the restriction map as shown in FIG. 9. It was revealed that as shown in FIG. 9 the DNA consisting of 2,316 base pairs encoding enzyme M-11 is located in the downstream near to the digested site by *Pst* I, a restriction enzyme.

Example 1-3

Production of enzyme by transformant

A liquid medium consisting of 2.0 w/v % maltose, 0.5 w/v % peptone, 0.1 w/v % yeast extract, 0.1 w/v % disodium hydrogen phosphate and 0.1 w/v % potassium dihydrogen phosphate was adjusted to pH 7.0, admixed with 50 µg/ml ampicillin, autoclaved at 120°C for 20 min, cooled and inoculated with a seed culture of transformant BMT7 obtained in Example 1-2, followed by culturing the transformant at 37°C for 24 hours with a rotary shaker. The resultant culture was treated with an ultrasonic disintegrator to disrupt cells, and the resultant suspension was centrifuged to remove insoluble substances. The supernatant thus obtained was assayed for the enzyme activity to find that one L of the culture yielded about 3,000 units of the enzyme.

As a control, a seed culture of *Escherichia coli* XLI-Blue or *Rhizobium* sp. M-11 was inoculated into a fresh preparation of the same liquid culture medium but free of ampicillin, and, in the case of the culture of *Rhizobium* sp. M-11, it was cultured and treated similarly as above except that the culturing temperature was set to 30°C.

Assaying the resultant activity, one L culture of *Rhizobium* sp. M-11 yielded about 1,500 units of the enzyme, and the yield was significantly lower than that of transformant BMT7. *Escherichia coli* XLI-Blue used as a host did not form the enzyme.

Thereafter, the enzyme produced by the transformant BMT7 purified similarly as in Experiment 1-1, and examined on the properties and characteristics. As a result, it was revealed that it has substantially the same physicochemical properties as that of Experiment 2 showing a molecular weight of about 76,000-87,000 daltons on SDS-PAGE and an isoelectric point of about 3.6-4.6 on isoelectrophoresis. The results indicate that the present enzyme can be prepared by recombinant DNA technology, and the yield is significantly increased thereby.

Example 2

Preparation of complementary DNA derived from enzyme M-11 and determination of its base sequence and amino acid sequence

Two µg of the recombinant DNA pBMT7 obtained by the method in Example 1-2 was weighed, admixed with 2 M aqueous sodium hydroxide solution to effect degeneration, and admixed with an adequate amount of cold ethanol, followed by collecting the resultant sediment containing a template DNA and drying the sediment in vacuo. To the template DNA were added 50 pmole/ml of a chemically synthesized primer 1 having the base sequence as shown in SEQ ID NO:7, and 10 µl of 40 mM Tris-HCl buffer (pH 7.5) containing 20 mM magnesium chloride and 50 mM sodium chloride, and incubated at 65°C for 2 min to effect annealing, and the mixture was admixed with 2 µl of an aqueous solution containing dATP, dGTP and dTTP in respective amounts of 7.5 µM, 0.5 µl of [α -³²P]dCTP (2 mCi/ml), one µl of 0.1 M dithiothreitol, and 2 µl of 1.5 units/ml T7 DNA polymerase, followed by incubating the resultant mixture at 25°C for 5 min to extend the primer 1 from the 5'-terminus to the 3'-terminus. Thus, a complementary chain DNA was formed.

The reaction product containing the complementary chain DNA was divided into quarters, to each of which 2.5 µl of 50 mM aqueous sodium chloride solution containing 80 µM dNTP and 8 µM ddATP, ddCTP, ddGTP or ddTTP was added, and the resultant mixture was incubated at 37°C for 5 min, followed by suspending the reaction by the addition of 4 µl of 95 v/v % aqueous formamide solution containing 20 mM EDTA, 0.05 w/v % bromophenol blue and 0.05 w/v % xylene cyanol. The reaction mixture was placed in a container, heated in a boiling-water bath for 3 min, placed on a gel containing 6 w/v % polyacrylamide, and electrophoresed by energizing the gel with a constant voltage of about 2,000 volts to separate DNA fragments, followed by fixing the gel in usual manner, drying and subjecting the resultant gel to autoradiography.

Analyses of the DNA fragments separated on the radiogram revealed that the complementary chain DNA contains the base sequence consisting of 2,936 base pairs as shown in SEQ ID NO:10. An amino acid sequence estimable from the base sequence was as shown in SEQ ID NO:10, and it was compared with the amino acid sequence containing the N-terminal and the partial amino acid sequence of enzyme M-11 as shown in SEQ ID NO:12, 14 or 15, and found that the amino acid sequence containing the N-terminal of SEQ ID NO:12 corresponded to the amino acid sequence at positions from 1 to 20 of SEQ ID NO:10, and the partial amino acid sequence of SEQ ID NO:14 or 15 corresponded to the amino acid sequence at positions from 486 to 506 or at positions from 606 to 626 of SEQ ID NO:10. The results indicate that the enzyme produced from *Rhizobium* sp. M-11 has the amino acid sequence of SEQ ID NO:2, and the enzyme derived from the microorganism is encoded by the DNA having the base sequence as shown in SEQ ID NO:1.

Example 3

Preparation of recombinant DNA containing DNA derived from *Arthrobacter* sp. Q36 and transformant

Example 3-1

Preparation of chromosomal DNA

Similarly as in Example 1-1, a chromosomal DNA was isolated from *Arthrobacter* sp. Q36, purified and dissolved in SSC buffer (pH 7.1) to give a concentration of about one mg/ml, and the resultant solution was frozen at -80°C.

Example 3-2Preparation of recombinant DNA pBQT13 and transformant BQT13

5 The purified chromosomal DNA obtained in Example 3-1 was partially digested similarly as in Example 1-2, followed by recovering a DNA fragment consisting of about 3,000-6,000 base pairs by sucrose density gradient ultracentrifugation. The DNA fragment was ligated to a lysate of Bluescript II SK(+) which had been treated with *Bam* HI similarly as in Example 1-2, and the resultant recombinant DNA was introduced into *Es-*
 10 *cherichia coli* XLI-Blue. The transformants thus obtained were cultured similarly as in Example 1-2 in an agar plate containing 5-bromo-4-chloro-3-indolyl- β -D-galactoside, and the resultant about 4,500 colonies were fixed on a nylon film, while probe 3 having the base sequence as shown in SEQ ID NO:8 was chemically synthesized based on the amino acid sequence as expressed by Phe-Asp-Val-Asp-Trp-Asp, which are located at positions from 11 to 16 in the amino acid sequence of the peptide fragment D as shown in SEQ ID NO:17, labelled with 32 P, and hybridized with transformant colonies which had been fixed on the nylon film, followed by selecting
 15 8 transformants which strongly hybridized with probe 3.

Similarly as in Example 1-2, the objective recombinant DNA was selected from the 8 transformants, and hybridized with probe 4 having the base sequence as shown in SEQ ID NO:9 which had been chemically synthesized based on the amino acid sequence located at positions from 16 to 20, i.e. Thr-Glu-Phe-Trp-Asp, in SEQ ID NO:16, followed by selecting a recombinant DNA which strongly hybridized with probe 4. The recombinant DNA and transformant thus selected were respectively named pBQT13 and BQT13.
 20

The transformant BQT13 was inoculated into L-broth containing ampicillin, and cultured similarly as in Example 3-2, and the proliferated cells were collected from the resultant culture, and from which a recombinant DNA was extracted, purified and analyzed to reveal that the recombinant pBQT13 consists of about 7,200 base pairs and has a structure expressed by the restriction map as shown in FIG. 10. As shown in FIG. 3, it was
 25 reveal that the DNA, which consists of 2,325 base pairs and encodes the DNA of enzyme Q36, is located in the downstream near the cleavage site of *Xmn* I.

Example 3-330 Production of enzyme by transformant BQT13

A liquid culture medium consisting of 2.0 w/v % maltose, 0.5 w/v % peptone, 0.1 w/v % yeast extract, 0.1 w/v % disodium hydrogen phosphate and 0.1 w/v % potassium dihydrogen phosphate was adjusted to pH 7.0, admixed with 50 μ g/ml ampicillin, autoclaved at 120°C for 20 min, cooled and inoculated with a seed culture
 35 of the transformant BQT13 obtained in Example 3-2, followed by culturing the transformant at 37°C for 24 hours by a rotary shaker. The resultant culture was treated with an ultrasonic disintegrator to disrupt cells, and the resultant suspension was centrifuged to remove insoluble substances. The supernatant thus obtained was assayed for the enzyme activity to find that one L of the culture yielded about 2,450 units of the enzyme.

As a control, *Escherichia coli* XLI-Blue or *Arthrobacter* sp. Q36 was inoculated in a fresh preparation of the same liquid culture medium but free of ampicillin, and cultured and treated similarly as above except that
 40 the culturing temperature was set to 30°C. The assay of the activity of the resultants showed that one L of the culture of *Arthrobacter* sp. Q36 yielded about 1,200 units of the enzyme, and the level of which was significantly lower than that of the transformant BQT13. *Escherichia coli* XLI-Blue used as a host did not form the enzyme.

Thereafter, the enzyme produced by the transformant BMT7 was purified similarly as in Experiment 1-1, and examined on the properties and characteristics. As a result, it was revealed that it has substantially the same physicochemical properties as shown in Experiment 2 of a molecular weight of about 76,000-87,000 daltons on SDS-PAGE and an isoelectric point of about 3.6-4.6 on isoelectrophoresis.

The results indicate that the enzyme can be prepared by recombinant DNA technology, and the yield might
 50 be significantly increased thereby.

Example 455 Preparation of complementary chain DNA derived from *Arthrobacter* sp. Q36, and determination of its base sequence and amino acid sequence

The recombinant DNA pBQT13 obtained in Example 3-2 was similarly treated as in Example 2 to form a template DNA which was then annealed together with the primer 1, followed by allowing T7 DNA polymerase

to act on the resultant to extend the primer 1 from the 5'-terminus to 3'-terminus to obtain a complementary chain DNA. Similarly as in Example 2, the complementary chain DNA was subjected to the dideoxy chain terminator method to analyze DNA fragments isolated on a radiogram. The result revealed that the complementary chain DNA contained a base sequence consisting of 3,073 base pairs and an amino acid sequence estimable from the base sequence were as shown in SEQ ID NO:11. The amino acid sequence was compared with respect to the amino acid sequence containing the N-terminal and the partial amino acid sequence of SEQ ID NO:13, 16 or 17, and found that the amino acid sequence containing the N-terminal of SEQ ID NO:13 corresponded to that located at positions from 1 to 20 in SEQ ID NO:11, and the partial amino acid sequence of SEQ ID NO:16 and 17 corresponded to the amino acid sequence located at positions from 606 to 625 or from 110 to 129 in SEQ ID NO:11. The results indicate that enzyme Q36 has the amino acid sequence of SEQ ID NO:4, and it is encoded by the DNA having the base sequence as shown in SEQ ID NO:3.

Example 5

Preparation of recombinant enzyme

In 500-ml Erlenmeyer flasks were placed 100 ml aliquots of a liquid culture medium (pH 7.0) consisting of 2.0 w/v % maltose, 0.5 w/v % peptone, 0.1 w/v % yeast extract, 0.1 w/v % disodium hydrogen phosphate and 0.1 w/v % potassium dihydrogen phosphate, and to each flask was added 50 µg/ml ampicillin and autoclaved at 120°C for 20 min. Thereafter, the flasks were cooled and inoculated with the transformant BMT7 obtained in Example 1-2, followed by culturing the transformant at 27°C for 24 hours by a rotary shaker. Apart from this, 18 L of a fresh preparation of the same liquid culture medium was placed in an Erlenmeyer flask, admixed with 50 µg/ml ampicillin, sterilized at 120°C for 20 min, cooled and inoculated with one v/v % of the seed culture obtained in the above, followed by the culture at 37°C for 24 hours under aeration and agitation conditions. The resultant culture was treated with an ultrasonic disintegrator to disrupt cells, and the resultant suspension was centrifuged to remove insoluble substances. The supernatant thus obtained was assayed for the enzyme activity to show that one L of the culture yielded about 3,000 units of the enzyme. The supernatant was purified by the method in Experiment 1-1 to obtain an about 50 ml aqueous solution containing about 135 units/ml of a recombinant enzyme having a specific activity of about 200 units/mg protein.

Example 6

Preparation of recombinant enzyme

Recombinant BQT13 obtained by the method in Example 3-2 was cultured similarly as in Example 5, and the resultant culture was treated with an ultrasonic integrator to disrupt cells. The resultant suspension was centrifuged to remove insoluble substances, and the resultant supernatant was assayed for the enzyme activity to reveal an enzyme production of about 2,450 units per L of the culture. The supernatant was purified by the method in Experiment 1-1 to obtain an about 45 ml aqueous solution containing about 120 units/ml of a recombinant enzyme having a specific activity of about 200 units/mg protein.

Example 7

Conversion of starch hydrolysate by recombinant enzyme

A potato starch was suspended in water to give a 6 w/w % suspension which was then autoclaved at 120°C for 10 min to gelatinize the starch. The gelatinized starch was rapidly cooled to 50°C, adjusted to a pH of about 4.5, admixed with 2,500 units/g starch, d.s.b., of an isoamylase specimen commercialized by Hayashibara Biochemical Laboratories, Inc., Okayama, Japan, and enzymatically reacted at 50°C for 20 hours. The reaction mixture was adjusted to pH 6.0, autoclaved at 120°C for 10 min to inactivate the remaining enzyme, rapidly cooled to 45°C, admixed with 150 units/g starch, d.s.b., of "TERMAMYL 60L", an α-amylase specimen commercialized by Novo Nordisk Bioindustri A/S, Copenhagen, Denmark, and enzymatically reacted at 45°C for 24 hours to obtain a reaction mixture containing reducing amylaceous saccharides having a degree of glucose polymerization of 3 or higher such as maltotriose, maltotetraose and maltopentaose. The reaction mixture was autoclaved at 120°C for 20 min to inactivate the remaining enzyme, rapidly cooled to 45°C, admixed with one unit/g starch, d.s.b., of the recombinant enzyme obtained in Example 5, and enzymatically reacted at 45°C for 96 hours. The resultant reaction mixture was heated at 96°C for 10 min to inactivate the remaining enzyme, cooled and filtered, and the resultant filtrate was in usual manner decolorized with an activated charcoal, de-

salted and purified by an ion exchanger and concentrated to obtain an about 70 w/w % syrup, d.s.b., in a yield of about 91%, d.s.b.

Analysis of the syrup conducted by the method of Experiment 2-1 revealed that it had a DE (dextrose equivalent) of 18.7 and contained as a main component, on a dry solid basis, 8.4 w/w % α -glucosyl trehalose, 5.6 w/w % α -maltosyl trehalose, 37.9 w/w % α -maltotriosyl trehalose, and that the greater part of the aforesaid reducing saccharides were converted into their corresponding non-reducing saccharides. The product, having a mild and moderate sweetness as well as an adequate viscosity and moisture-retaining ability, can be satisfactorily used in food products, cosmetics and pharmaceuticals as a sweetener, taste-improving agent, taste-improving agent, quality-improving agent, stabilizer, filler, excipient and adjuvant. The product contains non-reducing saccharides in a relatively-high content, so it can be also used as an intermediate for preparing trehalose.

Example 8

Conversion of starch hydrolysate by recombinant enzyme

Potato starch was suspended in water to give a concentration of 33 w/w %, d.s.b., and the suspension was admixed with 0.1 w/w % calcium carbonate, d.s.b. The resultant suspension was admixed with 0.2 w/w % per g starch, d.s.b., of "TERMAMYL 60L", an α -amylase specimen commercialized by Novo Nordisk Bioindustri A/S, Copenhagen, Denmark, and enzymatically reacted at 95°C for 15 min. The reaction mixture was autoclaved at 120°C for 10 min to inactivate the remaining enzyme, rapidly cooled, admixed with 5 units/g starch, d.s.b., of a maltotetraose-forming amylase derived from *Pseudomonas stutzeri* as disclosed in Japanese Patent Laid-Open No.240,784/88, and enzymatically reacted at 55°C for 6 hours. Thereafter, the resultant reaction mixture was admixed with 30 units/g starch, d.s.b., of " α -amylase 2A", an α -amylase specimen commercialized by Ueda Chemical Co., Ltd., Osaka, Japan, and enzymatically reacted at 65°C for 4 hours to form about 50 w/w %, d.s.b., of reducing amylaceous saccharides having a degree of glucose polymerization of 3 or higher such as maltotriose, maltotetraose and maltopentaose. The resultant mixture was autoclaved at 120°C for 10 min to inactivate the remaining enzyme, rapidly cooled to 45°C, adjusted to pH 6.5, admixed with 2 units/g amylaceous saccharide, d.s.b., of the recombinant enzyme obtained in Example 5, and enzymatically reacted at 45°C for 64 hours. The reaction mixture thus obtained was heated at 95°C for 10 min to inactivate the remaining enzyme, cooled, filtered, decolored in usual manner with an activated charcoal, desalted and purified with an ion exchanger, and concentrated to obtain a syrupy product with a concentration of about 70 w/w %, d.s.b., in a yield of about 90% against the material starch, d.s.b.

Analysis of the syrupy product by the method in Experiment 2-1 revealed that it had a DE of 10.5 and contained as a main component 3.8 w/w % α -glucosyl trehalose, 43.8 w/w % α -maltosyl trehalose, and 1.2 w/w % α -maltotriosyl trehalose, d.s.b., and that most of the reducing amylaceous saccharides contained therein were converted into their corresponding non-reducing saccharides. The product, having a mild and moderate sweetness as well as an adequate viscosity and moisture-retaining ability, can be satisfactorily used in food products, cosmetics and pharmaceuticals as a sweetener, taste-improving agent, quality-improving agent, stabilizer, filler, excipient and adjuvant. The product contains non-reducing saccharides in a relatively-high content, so it can be also used as an intermediate for preparing trehalose.

Example 9

Conversion of maltopentaose by recombinant enzyme

A high-purity maltopentaose produced by Hayashibara Biochemical Laboratories, Inc., Okayama, Japan, was dissolved in water to give a concentration of 20 w/w %, d.s.b., and the solution was adjusted to pH 6.5, admixed with one unit/g maltopentaose, d.s.b., of a recombinant enzyme obtained by the method in Example 5, and enzymatically reacted at 45°C for 48 hours. The reaction mixture was heated at 95°C for 10 min to inactivate the remaining enzyme, cooled, filtered, concentrated and analyzed by the method in Experiment 2-1 to find that about 92 w/w %, d.s.b., of the material maltopentaose was converted into α -maltotriosyl trehalose.

Four jacketed-stainless steel columns, having a diameter of 5.4 cm and a length of 5 m each, were packed to homogeneity with "XT-1016 (Na⁺-form)", a strong-acid cation exchange resin commercialized by Tokyo Organic Chemical Industries, Ltd., Tokyo, Japan, and cascaded in series to give a total column length of 20 m. The reaction mixture obtained in the above was fed to the columns at a rate of about 5 v/v % against the resin at an inner column temperature of 55°C, and the columns were fed with 55°C hot water at an SV (space velocity) of 0.13 to elute saccharide components. Based on the saccharide composition analysis of the eluate,

fractions rich in non-reducing saccharides were collected, pooled, concentrated, dried *in vacuo* and pulverized to obtain a solid product in a yield of about 55%, d.s.b.

Analysis of the solid product by the method in Experiment 2-1 revealed that it had a DE less than about 0.2 and contained 99.0 w/w % α -maltotriosyl trehalose, d.s.b. The product, having a relatively-low hygroscopicity, a significantly-low reducibility as well as a slight sweetness, can be satisfactorily used in food products, cosmetics and pharmaceuticals as a sweetener, taste-improving agent, quality-improving agent, stabilizer, filler, excipient and adjuvant. The product contains non-reducing saccharides in a relatively-high content, so it can be also used as an intermediate for preparing trehalose.

Example 10

Conversion of starch hydrolysate by recombinant enzyme

"PINE-DEX #4", a starch hydrolysate produced by Matsutani Chemical Ind., Co., Ltd., Kyoto, Japan, was dissolved in water to give a concentration of 40 w/w %, d.s.b., and the solution was heated to 45°C, adjusted to pH 6.5, admixed with one unit/g starch hydrolysate, d.s.b., of a recombinant enzyme obtained by the method in Example 5, and enzymatically reacted at for 96 hours to obtain a reaction mixture containing non-reducing saccharides having trehalose structure as an end unit. Thereafter, the reaction mixture was heated at 100°C for 10 min to inactivate the remaining enzyme, concentrated up to a 20 w/w % solution, d.s.b., cooled to 55°C, adjusted to pH 4.5, admixed with 10 units/g saccharide, d.s.b., of "GLUCOZYME", a glucoamylase specimen commercialized by Nagase Biochemicals, Ltd., Kyoto, Japan, and enzymatically reacted for 40 hours. The reaction mixture was heated at 100°C for 10 min to inactivate the remaining enzyme, cooled, decolorized in usual manner with an activated charcoal, desalted and purified with an ion exchanger, and concentrated to obtain an about 60 w/w % syrupy product containing about 29.7 w/w % trehalose, d.s.b.

Similarly as in Example 9 except for using "CG6000 (Na⁺-form)", the syrupy product was fractionated, followed by collecting fractions containing about 90 w/w % trehalose, d.s.b. The fractions were pooled, concentrated into an about 75 w/w % solution which was then transferred to a crystallizer, admixed with about 2 w/w % trehalose hydrate as a seed crystal against saccharides, d.s.b., and crystallized under gentle stirring conditions to obtain a masseccuite with a crystallinity of about 45%. The masseccuite was sprayed downward from a nozzle, equipped at the upper part of a spraying tower at a pressure of about 150 kg/cm² while about 85°C hot air was flowing downward from the upper part of the tower to accumulate a crystalline powder on a belt conveyer provided on the basement of the tower, followed by gradually transferring it out of the tower. Thereafter, the powder was transferred to an aging tower and aged for 10 hours to complete the crystallization and drying while an about 40°C hot air was blowing to the contents.

The product, having a substantial non-hygroscopicity and a mild and high-quality sweetness, can be satisfactorily used in food products, cosmetics, pharmaceuticals and feeds as a sweetener, taste-improving agent, quality-improving agent, stabilizer, filler, excipient and adjuvant.

Example 11

Conversion of starch hydrolysate by recombinant enzyme

Tapioca starch was suspended in water to give a concentration of 34 w/w % and admixed with 0.1 w/w % calcium carbonate. To the suspension was added 0.2 w/w % per g starch, d.s.b., of "TERMAMYL 60L", an α -amylase specimen commercialized by Novo Nordisk Bioindustri A/S, Copenhagen, Denmark, and enzymatically reacted at 95°C for 15 min to liquefy the starch. The liquefied product was autoclaved at 120°C for 10 min to inactivate the remaining enzyme, rapidly cooled to 55°C, adjusted to pH 5.2, admixed with 10 units/g starch, d.s.b., of " α -amylase 2A", an α -amylase specimen commercialized by Ueda Chemical Co., Ltd., Osaka, Japan, and 500 units of an isoamylase specimen commercialized by Hayashibara Biochemical Laboratories, Inc., Okayama, Japan, and enzymatically reacted at 55°C for 20 hours to form a mixture with a DE of about 29, containing about 60 w/w %, d.s.b., of reducing amylaceous saccharides having a degree of glucose polymerization of 3 or higher such as maltotriose, maltotetraose, maltopentaose and maltohexaose. The mixture was autoclaved at 120°C for 10 min to inactivate the remaining enzyme, rapidly cooled to 45°C, adjusted to pH 6.5, admixed with 2 units/g amylaceous saccharide, d.s.b., of a recombinant enzyme obtained by the method in Example 6, and enzymatically reacted at 45°C for 64 hours. The reaction mixture thus obtained was heated at 95°C for 10 min to inactivate the remaining enzyme, cooled, filtered, decolorized in usual manner with an activated charcoal, desalted and purified with an ion exchanger, and concentrated to obtain a syrupy product with a concentration of about 70 w/w %, d.s.b., in a yield of about 90% against the material starch, d.s.b.

Analysis of the syrupy product by the method in Experiment 2-1 revealed that it had a DE of 15.8 and contained as a main component 5.8 w/w % α -glucosyl trehalose, 8.5 w/w % α -maltoosyl trehalose, 13.1 w/w % α -maltotriosyl trehalose, 18.9 w/w % α -maltotetraosyl trehalose and 3.6 w/w % α -maltopentaosyl trehalose, d.s.b., and that most of the reducing amylaceous saccharides contained therein were converted into their corresponding non-reducing saccharides. The product, having a mild and moderate sweetness as well as an adequate viscosity and moisture-retaining ability, can be satisfactorily used in food products, cosmetics and pharmaceuticals as a sweetener, taste-improving agent, quality-improving agent, stabilizer, filler, excipient and adjuvant. The product contains non-reducing saccharides in a relatively-high content, so it can be also used as an intermediate for preparing trehalose.

Example 12

Conversion of starch hydrolysate by recombinant enzyme

Similarly as in Example 8, a liquefied potato starch was successively subjected to the action of maltotetraose-forming amylase and α -amylase to form a mixture containing about 50 w/w %, d.s.b. of reducing amylaceous saccharides having a degree of glucose polymerization of 3 or higher such as maltotriose, maltotetraose and maltopentaose. The reaction mixture was autoclaved at 120°C for 10 min to inactivate the remaining enzyme, rapidly cooled to 45°C, adjusted to pH 6.5, admixed with 2 units/g amylaceous saccharide, d.s.b., of a recombinant enzyme obtained by the method in Example 6, and enzymatically reacted at 45°C for 64 hours. The reaction mixture thus obtained was heated at 95°C for 10 min to inactivate the remaining enzyme, cooled and filtered, and the filtrate was decolorized in usual manner with an activated charcoal, desalted and purified with an ion exchanger, and concentrated to obtain an about 70 w/w % syrupy product in a yield of about 90 w/w % against the material starch, d.s.b.

Analysis of the syrupy product by the method in Experiment 2-1 revealed that it had a DE of 10.3 and contained as a main component 3.6 w/w % α -glucosyl trehalose, 44.0 w/w % α -maltoosyl trehalose and 1.0 w/w % α -maltotriosyl trehalose, d.s.b., and that most of the reducing amylaceous saccharides contained in the syrupy product were converted into their corresponding non-reducing saccharides. The product, having a mild and moderate sweetness as well as an adequate viscosity and moisture-retaining ability, can be satisfactorily used in food products, cosmetics and pharmaceuticals as a sweetener, taste-improving agent, quality-improving agent, stabilizer, filler, excipient and adjuvant. The product contains non-reducing saccharides in a relatively-high content, so it can be also used as an intermediate for preparing trehalose.

As is described above, the present invention is based on the finding of a novel enzyme which forms non-reducing saccharides having trehalose structure as an end unit from reducing saccharides having a degree of glucose polymerization of 3 or higher. The present invention is to explore a way to produce such enzyme by recombinant DNA technology in a relatively-large scale and in a considerably-high yield. The conversion method using the present recombinant enzyme effectively converts reducing amylaceous saccharides into their corresponding non-reducing saccharides which have a mild and high-quality sweetness and an adequate viscosity and moisture-retaining ability, do not have a reducing residue within the molecules, and sweeten food products without fear of causing an unsatisfactory coloration and deterioration. In addition, the present recombinant enzyme is the one with a revealed total amino acid sequence, and because of this it can be used for the preparation of trehalose and non-reducing saccharides having trehalose structure as an end unit which are premised on being used in food products without fear of causing side effects.

Thus, the present invention is a significant invention which exerts the aforesaid outstanding action and effect as well as giving a great contribution to the field.

While there has been described what is at present considered to be the preferred embodiments of the invention, it will be understood the various modifications may be made therein, and it is intended to cover in the appended claims all such modifications as fall within the true spirits and scope of the invention.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

NAME: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU
KENKYUJO

(ii) TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA
AND ENZYME, TRANSFORMANT, AND THEIR
PREPARATIONS AND USES.

(iii) NUMBER OF SEQUENCES: 17

(iv) ADDRESS:

(A) ADDRESSEE: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU
KAGAKU KENKYUJO

(B) STREET: 2-3, 1-CHOME, SHIMOISHII

(C) CITY: OKAYAMA

(E) COUNTRY: JAPAN

(F) POSTAL CODE (ZIP): 700

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(vii) PRIOR APPLICATION DATA:

(A1) APPLICATION NUMBER: JP 47940/1994

(B1) FILING DATE: February 23, 1994

(A2) APPLICATION NUMBER: JP 47956/1994

(B2) FILING DATE: February 23, 1994

(A3) APPLICATION NUMBER: JP 90705/1994

(B3) FILING DATE: April 6, 1994

(A4) APPLICATION NUMBER: JP 90728/1994

(B4) FILING DATE: April 6, 1994

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2316 base pairs

(B) TYPE: nucleic acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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ATCCTGAAGG	CAGAGAGCGG	CTCCGACCAC	GGCTATGACG	TCACCGATCC	CGCCGTAGTG	180
GACCCGGAGC	GCGGCGGCCC	TGAAGGGCTG	GCCGCGGTGT	CCAAGGCGGC	CCGCGGTGCC	240
GGCATGGGCG	TGCTGATCGA	CATCGTGCCG	AACCACGTGG	GCGTGCGGTC	GCCGCCGCAG	300
AACCCGTGGT	GGTGGTCGCT	GCTCAAGGAA	GGGCGCGGGT	CGCCCTACGC	CGTGGCGTTC	360
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GATCTGGACC	AGCTCGAAAT	CAAGGACGGC	GAGCTGCGGT	ACTACGACCA	CCGCTTCCCG	480
CTGGCCGAGG	GCAGCTACCG	GGACGGCGAC	TCCCCGCAGG	ACGTCCACGG	CCGGCAGCAC	540
TACGAAGTCA	TCCGCTGGCG	GCGGCCGGAC	AATGAAGTGA	ACTACCGCCG	GTTCTTCGCG	600
GTGAACACGC	TCGCCGGCAT	CCGGGTGGAG	GTGCCGCCGG	TCTTCGATGA	AGCGCACCAG	660
GAGGTGGTGC	GCTGGTTCCG	TGCGGGGCTC	GCCGACGGGC	TGCGGATCGA	CCACCCGGAC	720
GGCCTGGCCG	ATCCCGAGGG	GTATTTGAAG	CGGCTCCGTG	AGGTCACCGG	GGGCGCGTAC	780
CTGCTCATCG	AAAAGATCCT	CGAGCCGGGC	GAACAGTTGC	CGGCCAGCTT	CGAGTGCGAA	840
GGCACCACCG	GCTACGACGC	CCTCGCGGAT	GTCGACAGGG	TCTTCGTGGA	CCCGCGGGGA	900
CAGGTGCCGC	TGGACCGTCT	GGACGCACGG	CTGCGCGGCG	GTGCGCCGGC	CGACTACGAG	960
GACATGATCC	GCGGGACCAA	GCGCCGGATC	ACCGACGGCA	TCCTGCACTC	CGAGATCCTG	1020
CGCCTTGCCA	GGCTGGTGCC	CGAGCAGACC	GGAATTCCCG	GGGAGGCGGC	CGCGGATGCG	1080

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 20 ACCGGCTCCA CTTTCGGGCC GGGACCGGCG GCGCTGTCAG AAGTCTTCCG GGCCTACCCG 2280
 GTGGCCTTGT TGGTCCCCGC GACAGGAGGC AAGTCA 2316

(3) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 772

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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 20 25 30
 Trp Ile Tyr Leu Ser Pro Ile Leu Lys Ala Glu Ser Gly Ser Asp His Gly
 35 40 45 50
 Tyr Asp Val Thr Asp Pro Ala Val Val Asp Pro Glu Arg Gly Gly Pro Glu
 55 60 65
 Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Gly Ala Gly Met Gly Val Leu
 70 75 80 85
 Ile Asp Ile Val Pro Asn His Val Gly Val Ala Ser Pro Pro Gln Asn Pro
 90 95 100
 Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg Gly Ser Pro Tyr Ala Val Ala
 105 110 115
 Phe Asp Val Asp Trp Asp Leu Ala Gly Gly Arg Ile Arg Ile Pro Val Leu
 120 125 130 135
 Gly Ser Asp Asp Asp Leu Asp Gln Leu Glu Ile Lys Asp Gly Glu Leu Arg
 140 145 150
 Tyr Tyr Asp His Arg Phe Pro Leu Ala Glu Gly Ser Tyr Arg Asp Gly Asp
 155 160 165 170
 45 Ser Pro Gln Asp Val His Gly Arg Gln His Tyr Glu Leu Ile Gly Trp Arg
 175 180 185
 Arg Ala Asp Asn Glu Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu
 190 195 200
 Ala Gly Ile Arg Val Glu Val Pro Pro Val Phe Asp Glu Ala His Gln Glu
 205 210 215 220
 50 Val Val Arg Trp Phe Arg Ala Gly Leu Ala Asp Gly Leu Arg Ile Asp His
 225 230 235
 Pro Asp Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val
 240 245 250 255
 Thr Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln
 260 265 270

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	Glu	Phe	His	Val	Arg	Met	Ala	Arg	Arg	Gln	Ala	Glu	Leu	Pro	Leu	Ser	Met
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	Asp	Pro	Asp	Asn	Arg	Arg	Pro	Phe	Ser	Phe	Ala	Glu	Arg	Ile	Arg	Ala	Leu
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	Leu	Phe	Thr	Gly	Tyr	Arg	Pro	Val	His	Ala	Arg	Gly	Pro	Ala	Ala	Gly	His
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45	Leu	Val	Ala	Phe	Asp	Arg	Gly	Ala	Gly	Gly	Val	Leu	Ala	Leu	Ala	Thr	Arg
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	750					755						760				765	
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						770											

55 (4) INFORMATION FOR SEQ ID NO:3:
 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2325 base pairs

(B) TYPE: nucleic acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

5 ATGAGAACGC CAGTCTCCAC GTACAGGCTG CAGATCAGGA AGGGATTAC ACTCTTCGAC 60
 GCGGCCAAAA CCGTTCCGTA CCTGCACTCG CTCGGCGTCG ACTGGGTCTA CCTTTCTCCG 120
 10 GTCCTGACTG CCGAGCAGGG CTCCGACCAC GGGTACGACG TCACCGATCC CTCGCGCGTC 180
 GACCCCGAAC GCGGCGGGCC GGAGGGCCTC GCGGCGGTTT CCAAGGCGGC CCGCGCCGCG 240
 GGCATGGGCG TGCTGATCGA CATCGTGCCC AACCACGTGG GCGTCGCGAC GCCGGCGCAG 300
 AACCCCTGGT GGTGGTCGCT GCTCAAGGAG GGACGCCAGT CCCGTTACGC GGAGGCGTTC 360
 GACGTCGATT GGGACCTCGC CGGGGGACGC ATCCGGCTGC CGGTGCTCGG CAGCGACGAT 420
 GACCTCGACC AGCTCGAAAT CAGGGACGGG GAGCTGCGGT ACTACGACCA CCGATTCCCG 480
 CTCGCCGAGG GAACCTACGC CGAAGGCGAC GCCCGCGGGG ATGTCCACGC CCGGCAGCAC 540
 15 TACGAGCTCA TCGGCTGGCG CCGCGCGGAC AACGAGCTGA ACTACCGCCG CTTTTTCGCG 600
 GTGAACACGC TCGCCGGCGT CCGCGTGGAA ATCCCCGCGG TCTTCGACGA GGCACACCAG 660
 GAGGTGGTGC GCTGGTTCCG CGAGGACGGC TGCGGATCGA TGCGGATCGA GGCACACCAG 720
 GGCCTCGGCG ACCCGAGGG GTACCTGAAG CGACTCCGGG AAGTCAACGG CCGCGCTTAC 780
 CTGCTGATCG AAAAGATCCT GGAGCCGGGG GAGCAGCTGC CCGCCAGCTT CGAGTGTGAA 840
 GGCACCACAG GCTACGACGC CCTCGCCGAC GTCGACCGGG TTCTCGTGA CCCGCGCGGC 900
 20 CAGGAACCCG TGGACCGGCT TGACGCGTCC CTGCGTGGCG GCGAGCCCGC CGATTCCCG 960
 GACATGATCC CGCGAACCAG GCGCCGGAT ACCGACGGTA TCCTGCACTC GGAGATCCTG 1020
 CCGCTGGCCC GGCTGGTTCC GGGCGACGCC AACGTTTCAA TCGACGCCGG AGCCGACGCT 1080
 CTCGCCGAAA TCATCGCCGC CTTCCCGGTC TACCGCACCT ACCTGCCGGA GGGCGCCGAG 1140
 GTCCTGAAGG AGGCGTGCGA GCTTGCCGCG CGTAGGCGGC CGGAACCTGA CCAGGCCATC 1200
 CAGGCTCTGC AGCCGCTGCT GCTGGACACG GACCTCGAGC TTGCCCCGCG CTTCCAGCAG 1260
 25 ACCTCGGGCA TGGTCATGGC CAAGGGCGTG GAGGACACCG CGTTCTTCCG CTACAACCGC 1320
 CTGGGCACCC TCACGGAAGT GGGCGCCGAC CCCACCGAGT TCGCCGTGGA GCCGGACGAG 1380
 TTCCACGCCC GGCTGGCAGC CCGGCAGGCC GAGCTTCCGC TGTCCATGAC GACGCTGAGC 1440
 ACGCACGACA CCAAGCGCAG CGAGGACACC CGAGCAAGGA TTTCCGTGAT TTCCGAGGTT 1500
 GCGGGTGACT GGGAAAAGGC CTTGAACCGG CTGCGCGACC TGGCCCCGCT GCCGGACGGC 1560
 CCGCTGTCCG CGCTGCTCTG GCAGGCCATT GCCGGCGCCT GGCCCCGCA CCGGGAACGC 1620
 30 CTGCAGTACT ACGCGCTGAA GGCCGCGCGT GAAGCGGGGA ACTCGACCAA TGGGACCGAT 1680
 CCGGCCCCCG CGTTCGAGGA GAAGCTGAAG GCCGCGGTG ACGCCGTGTT CGACAATCCC 1740
 GCCGTGCAGG CCGAGGTGGA AGCCCTCGTC GAGCTCCTGG AGCCGTACGG AGCTTCGAAC 1800
 TCCCTCGCCG CCAAGCTCGT GCAGCTGACC ATGCCCGGCG TCCCGGACGT CTACCAGGGC 1860
 ACGGAGTTCT GGGACCGGTC GCTGACGGAC CCGGACAACC GCGGCGCGTT CAGCTTCGAG 1920
 GACCGCCGCG CCGCGCTGGA GCAGCTGGAT GCCGCGGACC TTCCCGCGTC ATTACCGAT 1980
 35 GAGCGGACGA AGCTGCTAGT GACGTCGCGC GCGCTGCGGC TGGCGCCGGA CCGTCCGGAG 2040
 CTGTTACGGG GGTACCGGCC GGTCTTGGCC AGCGGGCCCC CCGCCGGGCA CCTGCTCGCG 2100
 TTCGACCGCG GCACCGCGGC GCGCGCGGAT GCATTGACCC TCGCCACGCG GCTTCCCTAC 2160
 GGGCTGGAAC AGTCGGGTGG ATGGCGGGAC ACCGCGGTCG AACTTAACAC CGCCATGAAA 2220
 GACGAACTGA CCGGTGCCGG CTTCCGACCG GGGGCAGTGA AGATCGCCGA CATCTTCCGG 2280
 40 TCGTTCCCCG TTGCGCTGCT GGTGCCGCGC ACAGGAGGAG AGTCA 2325

(5) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 775

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

50 Met Arg Thr Pro Val Ser Thr Tyr Arg Leu Gln Ile Arg Lys Gly Phe Thr
 1 5 10 15
 Leu Phe Asp Ala Ala Lys Thr Val Pro Tyr Leu His Ser Leu Gly Val Asp
 20 25 30
 Trp Val Tyr Leu Ser Pro Val Leu Thr Ala Glu Gln Gly Ser Asp His Gly
 35 40 45 50
 Tyr Asp Val Thr Asp Pro Ser Ala Val Asp Pro Glu Arg Gly Gly Pro Glu
 55 60 65
 Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Ala Ala Gly Met Gly Val Leu
 70 75 80 85

5 Ile Asp Ile Val Pro Asn His Val Gly Val Ala Thr Pro Ala Gln Asn Pro
 90 95 100
 Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg Gln Ser Arg Tyr Ala Glu Ala
 105 110 115
 Phe Asp Val Asp Trp Asp Leu Ala Gly Gly Arg Ile Arg Leu Pro Val Leu
 120 125 130 135
 Gly Ser Asp Asp Asp Leu Asp Gln Leu Glu Ile Arg Asp Gly Glu Leu Arg
 140 145 150
 10 Tyr Tyr Asp His Arg Phe Pro Leu Ala Glu Gly Thr Tyr Ala Glu Gly Asp
 155 160 165 170
 Ala Pro Arg Asp Val His Ala Arg Gln His Tyr Glu Leu Ile Gly Trp Arg
 175 180 185
 Arg Ala Asp Asn Glu Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu
 190 195 200
 15 Ala Gly Val Arg Val Glu Ile Pro Ala Val Phe Asp Glu Ala His Gln Glu
 205 210 215 220
 Val Val Arg Trp Phe Arg Glu Asp Leu Ala Asp Gly Leu Arg Ile Asp His
 225 230 235
 Pro Asp Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val
 240 245 250 255
 20 Thr Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln
 260 265 270
 Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu Ala
 275 280 285
 Asp Val Asp Arg Val Leu Val Asp Pro Arg Gly Gln Glu Pro Leu Asp Arg
 290 295 300 305
 25 Leu Asp Ala Ser Leu Arg Gly Gly Glu Pro Ala Asp Tyr Gln Asp Met Ile
 310 315 320 325
 Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His Ser Glu Ile Leu
 325 330 335 340
 Arg Leu Ala Arg Leu Val Pro Gly Asp Ala Asn Val Ser Ile Asp Ala Gly
 345 350 355
 30 Ala Asp Ala Leu Ala Glu Ile Ile Ala Ala Phe Pro Val Tyr Arg Thr Tyr
 360 365 370
 Leu Pro Glu Gly Ala Glu Val Leu Lys Glu Ala Cys Glu Leu Ala Ala Arg
 375 380 385 390
 Arg Arg Pro Glu Leu Asp Gln Ala Ile Gln Ala Leu Gln Pro Leu Leu Leu
 395 400 405
 35 Asp Thr Asp Leu Glu Leu Ala Arg Arg Phe Gln Gln Thr Ser Gly Met Val
 410 415 420 425
 Met Ala Lys Gly Val Glu Asp Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly
 430 435 440
 Thr Leu Thr Glu Val Gly Ala Asp Pro Thr Glu Phe Ala Val Glu Pro Asp
 445 450 455
 40 Glu Phe His Ala Arg Leu Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met
 460 465 470 475
 Thr Thr Leu Ser Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg
 480 485 490
 Ile Ser Val Ile Ser Glu Val Ala Gly Asp Trp Glu Lys Ala Leu Asn Arg
 495 500 505 510
 45 Leu Arg Asp Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Ala Leu Leu Trp
 515 520 525
 Gln Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Tyr Tyr
 530 535 540
 Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Asn Trp Thr Asp Pro
 545 550 555 560
 50 Ala Pro Ala Phe Glu Glu Lys Leu Lys Ala Ala Val Asp Ala Val Phe Asp
 565 570 575
 Asn Pro Ala Val Gln Ala Glu Val Glu Ala Leu Val Glu Leu Leu Glu Pro
 580 585 590 595
 Tyr Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln Leu Thr Met Pro
 600 605 610
 55 Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp Asp Arg Ser Leu Thr
 615 620 625

Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Asp Asp Arg Arg Ala Ala Leu
 630 635 640 645
 5 Glu Gln Leu Asp Ala Gly Asp Leu Pro Ala Ser Phe Thr Asp Glu Arg Thr
 650 655 660
 Lys Leu Leu Val Thr Ser Arg Ala Leu Arg Leu Arg Arg Asp Arg Pro Glu
 665 670 675 680
 Leu Phe Thr Gly Tyr Arg Pro Val Leu Ala Ser Gly Pro Ala Ala Gly His
 685 690 695
 10 Leu Leu Ala Phe Asp Arg Gly Thr Ala Ala Ala Pro Gly Ala Leu Thr Leu
 700 705 710
 Ala Thr Arg Leu Pro Tyr Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr
 715 720 725 730
 Ala Val Glu Leu Asn Thr Ala Met Lys Asp Glu Leu Thr Gly Ala Gly Phe
 735 740 745
 15 Gly Pro Gly Ala Val Lys Ile Ala Asp Ile Phe Arg Ser Phe Pro Val Ala
 750 755 760 765
 Leu Leu Val Pro Gln Thr Gly Gly Glu Ser
 770 775

20

(6) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH:14 base pairs
 (B) TYPE:nucleic acid
 25 (C) STRANDEDNESS:single
 (D) TOPOLOGY:unknown
 (ii) MOLECULE TYPE:other nucleic acid
 (A) probe

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCNGARTGGG ARAA

14

35

(7) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH:14 base pairs
 (B) TYPE:nucleic acid
 (C) STRANDEDNESS:single
 40 (D) TOPOLOGY:unknown
 (ii) MOLECULE TYPE:other nucleic acid
 (A) probe

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ACNGARTTYT GGGA

14

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(8) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH:17 base pairs
 (B) TYPE:nucleic acid
 (C) STRANDEDNESS:single
 (D) TOPOLOGY:unknown
 55 (ii) MOLECULE TYPE:other nucleic acid
 (A) primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GTAAAACGAC GGCCAGT

(9) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH:17 base pairs
- (B) TYPE:nucleic acid
- (C) STRANDEDNESS:single
- (D) TOPOLOGY:unknown

(ii) MOLECULE TYPE:other nucleic acid

(A) probe

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TTYGAYGTNG AYTGGGA

(10) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH:14 base pairs
- (B) TYPE:nucleic acid
- (C) STRANDEDNESS:single
- (D) TOPOLOGY:unknown

(ii) MOLECULE TYPE:other nucleic acid

(A) probe

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:9:

ACNGARTTYT GGGA

(11) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH:2936 base pairs
- (B) TYPE:nucleic acid
- (C) strandedness:double
- (D) TOPOLOGY:linear

(ii) MOLECULE TYPE:genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:Rhizobium sp.
- (B) INDIVIDUAL ISOLATE:M-11 (FERM BP-4130)

(ix) FEATURE:

- (A) NAME/KEY:5'UTR
- (B) LOCATION:1..564
- (C) IDENTIFICATION METHOD:E
- (A) NAME/KEY:mat peptide
- (B) LOCATION:565..2880
- (C) IDENTIFICATION METHOD:S
- (A) NAME/KEY:3'UTR
- (B) LOCATION:2881..2936
- (C) IDENTIFICATION METHOD:E

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:10:

CGTGCTCTAC	TTCAACGCGC	ACGACGGCGA	CGTCGTGTTT	AAGCTCCCGT	CGGATGAATA	60
CGCCCCGGCC	TGGGACGTCA	TCATCGACAC	CGCCGGCGCG	GGTGCCGATT	CCGAACCCGT	120
GCAGGCTGGC	GGCAAACCTCA	CCGTGGCAGC	GAAATCGCTC	GTGGTGCTCC	GTGCCCCACAG	180
CGCCCCGGAG	GAGGAACCGG	ACCACTCGGT	GGCCGCCTCC	CTCGCAGCGC	TGACGCAGAC	240
TGCGACCGCC	GAAACGCGG	CGTCCACCGC	CCCCACCGTT	CCGGAGCCGA	GGAAGACCAA	300

5	GAAGGCAGCG	CCGAAGCCGG	AAGAGGAGGC	TCCCGACGAG	GCGGCGCCGA	AGCCGGAAGA	360
	GAAGGCTCCC	GACGAGGCGG	CGGCGAAGCC	GGAAGAGGCT	GCTTCCGACG	AGGCGGCGGC	420
	GAAGCCGGAA	GAGAAGGCTC	CCGACGAGGC	GGCGGCAGAA	CCGGAAGAGG	CTGCTTCCGA	480
	CGAGGCGGCG	GCGAAGCCCG	CGGGGAAGGC	AGCGGCCAAA	ACGGCCGGCA	GGCGAGCGCC	540
	AGGCAAGCAG	GGCGGGACGG	GCTC				564
10	ATG AGG ACA	CCC GCC TCG	ACC TAC	CGG CTG CAG	ATC AGG CGG	GGT TTC	612
	Met Arg Thr	Pro Ala Ser	Thr Tyr Arg	Leu Gln Ile	Arg Arg Gly	Phe	
	1	5	10	15	20	25	
	ACG CTG TTT	GAT GCC GCC	GAG ACC GTG	CCC TAC CTG	AAG TCA CTC	GGG	660
	Thr Leu Phe	Asp Ala Ala	Glu Thr Val	Pro Tyr Leu	Lys Ser Leu	Gly	
15	GTG GAC TGG	ATC TAC CTG	TCG CCC	ATC CTG AAG	GCA GAG AGC	GGC TCC	708
	Val Asp Trp	Ile Tyr Leu	Ser Pro Ile	Leu Lys Ala	Glu Ser Gly	Ser	
	35	40	45	50	55	60	
	GAC CAC GGC	TAT GAC GTC	ACC GAT CCC	GCC GTA GTG	GAC CCG GAG	CGC	756
	Asp His Gly	Tyr Asp Val	Thr Asp Pro	Ala Val Val	Asp Pro Glu	Arg	
20	GGC GGC CCT	GAA GGG CTG	GCC GCG GTG	TCC AAG GCG	GCC CGC GGT	GCC	804
	Gly Gly Pro	Glu Gly Leu	Ala Ala Val	Ser Lys Ala	Ala Arg Gly	Ala	
	65	70	75	80	85	90	
	GGC ATG GGC	GTG CTG ATC	GAC ATC GTG	CCG AAC CAC	GTG GGC GTG	GCG	852
	Gly Met Gly	Val Leu Ile	Asp Ile Val	Pro Asn His	Val Gly Val	Ala	
25	TCG CCG CCG	CAG AAC CCG	TGG TGG TGG	TCG CTG CTC	AAG GAA GGC	CGC	900
	Ser Pro Pro	Gln Asn Pro	Trp Trp Trp	Ser Leu Leu	Lys Glu Gly	Arg	
	100	105	110	115	120	125	
	GGG TCG CCC	TAC GCC GTG	GCG TTC GAC	GTC GAC TGG	GAC CTG GCG	GGG	948
	Gly Ser Pro	Tyr Ala Val	Ala Phe Asp	Val Asp Trp	Asp Leu Ala	Gly	
30	GGC CGC ATC	CGG ATC CCC	GTC CTG GGC	AGC GAC GAC	GAT CTG GAC	CAG	996
	Gly Arg Ile	Arg Ile Pro	Val Leu Gly	Ser Asp Asp	Asp Leu Asp	Gln	
	130	135	140	145	150	155	
	CTC GAA ATC	AAG GAC GGC	GAG CTG CGG	TAC TAC GAC	CAC CGC TTC	CCG	1044
	Leu Glu Ile	Lys Asp Gly	Glu Leu Arg	Tyr Tyr Asp	His Arg Phe	Pro	
35	CTG GCC GAG	GGC AGC TAC	CGG GAC GGC	GAC TCC CCG	CAG GAC GTC	CAC	1092
	Leu Ala Glu	Gly Ser Tyr	Arg Asp Gly	Asp Ser Pro	Gln Asp Val	His	
	160	165	170	175	180	185	
	GGC CGG CAG	CAC TAC GAA	CTC ATC GGC	TGG CGG CGC	GCC GAC AAT	GAA	1140
	Gly Arg Gln	His Tyr Glu	Leu Ile Gly	Trp Arg Arg	Ala Asp Asn	Glu	
40	CTG AAC TAC	CGC CGG TTC	TTC GCG GTG	AAC ACG CTC	GCC GGC ATC	CGG	1188
	Leu Asn Tyr	Arg Arg Phe	Phe Ala Val	Asn Thr Leu	Ala Gly Ile	Arg	
	190	195	200	205	210	215	
	GTG GAG GTG	CCG CCG GTC	TTC GAT GAA	GCG CAC CAG	GAG GTG GTG	CGC	1236
	Val Glu Val	Pro Pro Val	Phe Asp Glu	Ala His Gln	Glu Val Val	Arg	
45	TGG TTC CGT	GCG GGG CTC	GCC GAC GGG	CTG CGG ATC	GAC CAC CCG	GAC	1284
	Trp Phe Arg	Ala Gly Leu	Ala Asp Gly	Leu Arg Ile	Asp His Pro	Asp	
	220	225	230	235	240	245	
	GGC CTG GCC	GAT CCC GAG	GGG TAT TTG	AAG CGG CTC	CGT GAG GTC	ACC	1332
	Gly Leu Ala	Asp Pro Glu	Gly Tyr Leu	Lys Arg Leu	Arg Glu Val	Thr	
50	GGG GGC GCG	TAC CTG CTC	ATC GAA AAG	ATC CTC GAG	CCG GGC GAA	CAG	1380
	Gly Gly Ala	Tyr Leu Leu	Ile Glu Lys	Ile Leu Glu	Pro Gly Glu	Gln	
	250	255	260	265	270	275	
	TTG CCG GCC	AGC TTC GAG	TGC GAA GGC	ACC ACC GGC	TAC GAC GCC	CTC	1428
	Leu Pro Ala	Ser Phe Glu	Cys Glu Gly	Thr Thr Gly	Tyr Asp Ala	Leu	
55	GCG GAT GTC	GAC AGG GTC	TTC GTG GAC	CCG CGG GGA	CAG GTG CCG	CTG	1476
	Ala Asp Val	Asp Arg Val	Phe Val Asp	Pro Arg Gly	Gln Val Pro	Leu	
	280	285	290	295	300		
	GAC CGT CTG	GAC GCA CGG	CTG CGC GGC	GGT GCG CCG	GCC GAC TAC	GAG	1524

	Asp	Arg	Leu	Asp	Ala	Arg	Leu	Arg	Gly	Gly	Ala	Pro	Ala	Asp	Tyr	Glu	
5	305					310					315					320	
	GAC	ATG	ATC	CGC	GGG	ACC	AAG	CGC	CGG	ATC	ACC	GAC	GGC	ATC	CTG	CAC	1572
	Asp	Met	Ile	Arg	Gly	Thr	Lys	Arg	Arg	Ile	Thr	Asp	Gly	Ile	Leu	His	
					325					330					335		
	TCC	GAG	ATC	CTG	CGC	CTT	GCC	AGG	CTG	GTG	CCC	GAG	CAG	ACC	GGA	ATT	1620
	Ser	Glu	Ile	Leu	Arg	Leu	Ala	Arg	Leu	Val	Pro	Glu	Gln	Thr	Gly	Ile	
10					340					345					350		
	CCC	GGG	GAG	GCG	GCC	GCG	GAT	GCG	ATC	GCG	GAG	ATC	ATC	GCG	GCC	TTC	1668
	Pro	Gly	Glu	Ala	Ala	Ala	Asp	Ala	Ile	Ala	Glu	Ile	Ile	Ala	Ala	Phe	
					355					360					365		
	CCG	GTC	TAC	CGG	TCC	TAT	CTT	CCC	GAG	GGC	GCG	GAG	ATC	CTG	AAG	GAG	1716
	Pro	Val	Tyr	Arg	Ser	Tyr	Leu	Pro	Glu	Gly	Ala	Glu	Ile	Leu	Lys	Glu	
					370					375					380		
15	GCC	TGC	GAC	CTC	GCC	GCG	CGG	AGG	CGT	CCG	GAA	CTG	GGC	CAG	ACC	GTC	1764
	Ala	Cys	Asp	Leu	Ala	Ala	Arg	Arg	Arg	Pro	Glu	Leu	Gly	Gln	Thr	Val	
					385					390					400		
	CAG	CTG	CTG	CAG	CCG	CTG	CTG	CTG	GAT	ACC	GAC	CTC	GAG	ATT	TCC	CGC	1812
	Gln	Leu	Leu	Gln	Pro	Leu	Leu	Leu	Asp	Thr	Asp	Leu	Glu	Ile	Ser	Arg	
					405					410					415		
20	AGG	TTC	CAG	CAG	ACC	TCG	GGA	ATG	GTC	ATG	GCC	AAA	GGC	GTG	GAG	GAC	1860
	Arg	Phe	Gln	Gln	Thr	Ser	Gly	Met	Val	Met	Ala	Lys	Gly	Val	Glu	Asp	
					420					425					430		
	ACC	GCG	TTC	TTC	CGC	TAC	AAC	CGG	CTG	GGA	ACG	CTC	ACC	GAG	GTG	GGC	1908
	Thr	Ala	Phe	Phe	Arg	Tyr	Asn	Arg	Leu	Gly	Thr	Leu	Thr	Glu	Val	Gly	
					435					440					445		
25	GCC	GAC	CCC	ACC	GAG	TTC	TCG	CTG	GAA	CCG	GAG	GAG	GAG	TTT	CAC	GTC	1956
	Ala	Asp	Pro	Thr	Glu	Phe	Ser	Leu	Glu	Pro	Glu	Glu	Phe	His	Val	Arg	
					450					455					460		
	ATG	GCC	CGC	CGG	CAG	GCC	GAA	CTC	CCG	CTC	TCC	ATG	ACC	ACC	CTG	AGC	2004
	Met	Ala	Arg	Arg	Gln	Ala	Glu	Leu	Pro	Leu	Ser	Met	Thr	Thr	Leu	Ser	
					465					470					475		
30	ACG	CAC	GAC	ACC	AAG	CGC	AGC	GAG	GAC	ACC	CGG	GCC	CGG	ATC	TCG	GTG	2052
	Thr	His	Asp	Thr	Lys	Arg	Ser	Glu	Asp	Thr	Arg	Ala	Arg	Ile	Ser	Val	
					485					490					495		
	ATC	GCC	GAG	GTC	GCG	CCT	GAA	TGG	GAA	AAG	GCC	CTG	GAC	AGG	CTG	AAC	2100
	Ile	Ala	Glu	Val	Ala	Pro	Glu	Trp	Glu	Lys	Ala	Leu	Asp	Arg	Leu	Asn	
					500					505					510		
35	ACC	CTC	GCT	CCG	CTG	CCG	GAC	GGC	CCG	CTC	TCC	ACG	CTG	CTC	TGG	CAG	2148
	Thr	Leu	Ala	Pro	Leu	Pro	Asp	Gly	Pro	Leu	Ser	Thr	Leu	Leu	Trp	Gln	
					515					520					525		
	GCG	ATT	GCG	GGG	GCA	TGG	CCG	GCC	AGC	CGG	GAA	CGC	CTT	CAG	TCC	TAC	2196
	Ala	Ile	Ala	Gly	Ala	Trp	Pro	Ala	Ser	Arg	Glu	Arg	Leu	Gln	Ser	Tyr	
					530					535					540		
40	GCC	CTG	AAA	GCG	GCG	CGC	GAA	GCC	GGG	AAC	TCG	ACC	AGC	TGG	ACC	GAT	2244
	Ala	Leu	Lys	Ala	Ala	Arg	Glu	Ala	Gly	Asn	Ser	Thr	Ser	Trp	Thr	Asp	
					545					550					555		
	CCG	GAC	CCG	GCA	TTC	GAG	GCA	CTT	TCC	GCC	GTC	GTC	GAC	TCC	GCC		2292
	Pro	Asp	Pro	Ala	Phe	Glu	Glu	Ala	Leu	Ser	Ala	Val	Val	Asp	Ser	Ala	
					565					570					575		
45	TTC	GAC	AAT	CCG	GAG	GTG	CGT	GCG	GAA	CTT	GAG	GCC	CTG	GTG	GGC	CTC	2340
	Phe	Asp	Asn	Pro	Glu	Val	Arg	Ala	Glu	Leu	Glu	Ala	Leu	Val	Gly	Leu	
					580					585					590		
	CTT	GCG	CCG	CAC	GGT	GCG	TCC	AAC	TCG	CTC	GCG	GCA	AAG	CTT	GTC	CAG	2388
	Leu	Ala	Pro	His	Gly	Ala	Ser	Asn	Ser	Leu	Ala	Ala	Lys	Leu	Val	Gln	
					595					600					605		
50	CTG	ACC	ATG	CCG	GGC	GTT	CCG	GAC	GTG	TAC	CAG	GGC	ACC	GAG	TTC	TGG	2436
	Leu	Thr	Met	Pro	Gly	Val	Pro	Asp	Val	Tyr	Gln	Gly	Thr	Glu	Phe	Trp	
					610					615					620		
	GAC	AGG	TCG	CTG	ACC	GAT	CCG	GAC	AAC	CGG	CGC	CCC	TTC	AGC	TTC	GCC	2484
	Asp	Arg	Ser	Leu	Thr	Asp	Pro	Asp	Asn	Arg	Arg	Pro	Phe	Ser	Phe	Ala	
					625					630					635		
	GAA	CGG	ATT	AGG	GCC	TTG	GAC	CAG	TTG	GAC	GCC	GGC	CAC	CGT	CCG	GAC	2532
55	Glu	Arg	Ile	Arg	Ala	Leu	Asp	Gln	Leu	Asp	Ala	Gly	His	Arg	Pro	Asp	

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5      TCC TTC CAG GAC 645 GAG GCG GTC AAG CTG 650 GTC ACC TCG AGG 655 GCG CTG 2580
      Ser Phe Gln Asp Glu Ala Val Lys Leu Leu Val Thr Ser Arg Ala Leu
      CGG CTG CGG CGG AAC CGG CCC GAG CTC TTC ACC GGC TAC CGC CCC GTG 2628
      Arg Leu Arg Arg Asn Arg Pro Glu Leu Phe Thr Gly Tyr Arg Pro Val
      CAT GCC AGG GGC CCC GCC GCC GGG CAC CTG GTG GCG TTC GAC CGC GGC 2676
10     His Ala Arg Gly Pro Ala Ala Gly His Leu Val Ala Phe Asp Arg Gly
      GCC GGG GGA GTG CTG GCG CTT GCC ACC CGG CTC CCC TAC GGG CTG GAA 2724
      Ala Gly Gly Val Leu Ala Leu Ala Thr Arg Leu Pro Tyr Gly Leu Glu
      CAG TCG GGC GGC TGG CGG GAC ACC GCC GTC GAG CTT GAA GCC GCC ATG 2772
15     Gln Ser Gly Gly Trp Arg Asp Thr Ala Val Glu Leu Glu Ala Ala Met
      ACG GAC GAA CTG ACC GGC TCC ACT TTC GGG CCG GGA CCG GCG GCG CTG 2820
      Thr Asp Glu Leu Thr Gly Ser Thr Phe Gly Pro Gly Pro Ala Ala Leu
      TCA GAA GTC TTC CGG GCC TAC CCG GTG GCC TTG TTG GTC CCC GCG ACA 2868
20     Ser Glu Val Phe Arg Ala Tyr Pro Val Ala Leu Leu Val Pro Ala Thr
      GGA GGC AAG TCA 2880
      Gly Gly Lys Ser
      TGACGCAGCC CAACGATGCG GCCAAGCCGG TGCAGGGAGC GGGGCGCTTC GATATC 2936

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(12) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3084 base pairs
- (B) TYPE: nucleic acid
- (C) strandedness: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Arthrobacter* sp.
- (B) INDIVIDUAL ISOLATE: Q36 (FERM BP-4316)

(ix) FEATURE:

- (A) NAME/KEY: 5' UTR
- (B) LOCATION: 1..677
- (C) IDENTIFICATION METHOD: E
- (A) NAME/KEY: mat peptide
- (B) LOCATION: 678..3002
- (C) IDENTIFICATION METHOD: S
- (A) NAME/KEY: 3' UTR
- (B) LOCATION: 3003..3073
- (C) IDENTIFICATION METHOD: E

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

```

45     GATCCGGACG GCAACCTCAT GTCCCCGGAG GACTGGGACA GCGGCTTCGG CCGTTCGGTG 60
      GGCATGTTCC TCAACGCGCA CGGCATCCAG GGCCACGATG ACCGCGGCCG CCGCATCACG 120
      GACGTGAACT TCCTGCTGTA CTTCAACGCC CACGACGGCG ACCTCGAGTT CACGCTGCCG 180
      CCGGACGAAT ACGCCCCGCG CTGGGACGTC ATCATCGACA CCGCCGGTGA AGGGGCGGAC 240
      TCCAAGCCCG CGGACGCCGG AACCATCCTG TCCGTTGCGG CCAAGTCGCT GGTGTGCTT 300
      CGCGCCACA GCGCACCAGA GGAGGAGCCT GACCATTCCG TGGCTGCTTC CCTGGCTGCA 360
      CTGACGCAGA CCGCCACCGC CGAGACGGCG GCGCTCACAG CTCCTGCCGT TCCCAGCCG 420
50     GCCAAGACGA AGAAGCCGCG CGTGACCCG GTTGCTGAAC CGGCCGACCC CGCGGTTGCT 480
      GACCCGGCCG ACCCGGTTGC TGACCCGGTT GCTGACCCGG CGCCGGAACC GGCTGCGGAG 540
      CCTGCGAAAT CCGCAGCGGA ACCTGGTGCG GAGCCTGCGA AGGACCCGGA GGAGCAGCCG 600
      GCGGAAAAGC CGGCGCGCAA GCCTGCGGCA AAGCGCGGCG GCCACCTGAG GCGGTCGAAG 660
      CCCGCTGGGG AGGACGC 677
      ATG AGA ACG CCA GTC TCC ACG TAC AGG CTG CAG ATC AGG AAG GGA TTC 725
80     Met Arg Thr Pro Val Ser Thr Tyr Arg Leu Gln Ile Arg Lys Gly Phe

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	1				5					10					15		
5	ACA	CTC	TTC	GAC	GCG	GCC	AAA	ACC	GTT	CCG	TAC	CTG	CAC	TCG	CTC	GGC	773
	Thr	Leu	Phe	Asp	Ala	Ala	Lys	Thr	Val	Pro	Tyr	Leu	His	Ser	Leu	Gly	
				20					25					30			
	GTC	GAC	TGG	GTC	TAC	CTT	TCT	CCG	GTC	CTG	ACT	GCC	GAG	CAG	GGC	TCC	821
	Val	Asp	Trp	Val	Tyr	Leu	Ser	Pro	Val	Leu	Thr	Ala	Glu	Gln	Gly	Ser	
			35					40				45					
10	GAC	CAC	GGG	TAC	GAC	GTC	ACC	GAT	CCC	TCC	GCC	GTC	GAC	CCC	GAA	CGC	869
	Asp	His	Gly	Tyr	Asp	Val	Thr	Asp	Pro	Ser	Ala	Val	Asp	Pro	Glu	Arg	
		50					55				60						
	GGC	GGG	CCG	GAG	GGC	CTC	GCG	GCG	GTT	TCC	AAG	GCG	GCC	CGC	GCC	GCG	917
	Gly	Gly	Pro	Glu	Gly	Leu	Ala	Ala	Val	Ser	Lys	Ala	Ala	Arg	Ala	Ala	
	65				70					75					80		
	GGC	ATG	GGC	GTG	CTG	ATC	GAC	ATC	GTG	CCC	AAC	CAC	GTG	GGC	GTC	GCG	965
15	Gly	Met	Gly	Val	Leu	Ile	Asp	Ile	Val	Pro	Asn	His	Val	Gly	Val	Ala	
				85					90					95			
	ACG	CCG	GCG	CAG	AAC	CCC	TGG	TGG	TGG	TCG	CTG	CTC	AAG	GAG	GGA	CGC	1013
	Thr	Pro	Ala	Gln	Asn	Pro	Trp	Trp	Trp	Ser	Leu	Leu	Lys	Glu	Gly	Arg	
				100				105					110				
20	CAG	TCC	CGT	TAC	GCG	GAG	GCG	TTC	GAC	GTC	GAT	TGG	GAC	CTC	GCC	GGG	1061
	Gln	Ser	Arg	Tyr	Ala	Glu	Ala	Phe	Asp	Val	Asp	Trp	Asp	Leu	Ala	Gly	
			115				120				125						
	GGA	CGC	ATC	CGG	CTG	CCG	GTG	CTC	GGC	AGC	GAC	GAT	GAC	CTC	GAC	CAG	1109
	Gly	Arg	Ile	Arg	Leu	Pro	Val	Leu	Gly	Ser	Asp	Asp	Asp	Leu	Asp	Gln	
		130				135					140						
25	CTC	GAA	ATC	AGG	GAC	GGG	GAG	CTG	CGG	TAC	TAC	GAC	CAC	CGA	TTC	CCG	1157
	Leu	Glu	Ile	Arg	Asp	Gly	Glu	Leu	Arg	Tyr	Tyr	Asp	His	Arg	Phe	Pro	
		145				150				155					160		
	CTC	GCC	GAG	GGA	ACC	TAC	GCC	GAA	GGC	GAC	GCC	CCG	CGG	GAT	GTC	CAC	1205
	Leu	Ala	Glu	Gly	Thr	Tyr	Ala	Glu	Gly	Asp	Ala	Pro	Arg	Asp	Val	His	
				165				170						175			
30	GCC	CGG	CAG	CAC	TAC	GAG	CTC	ATC	GGC	TGG	CGC	CGC	GCG	GAC	AAC	GAG	1253
	Ala	Arg	Gln	His	Tyr	Glu	Leu	Ile	Gly	Trp	Arg	Arg	Ala	Asp	Asn	Glu	
				180				185					190				
	CTG	AAC	TAC	CGC	CGC	TTT	TTC	GCG	GTG	AAC	ACG	CTC	GCC	GGC	GTC	CGC	1301
	Leu	Asn	Tyr	Arg	Arg	Phe	Phe	Ala	Val	Asn	Thr	Leu	Ala	Gly	Val	Arg	
			195				200					205					
35	GTG	GAA	ATC	CCC	GCC	GTC	TTC	GAC	GAG	GCA	CAC	CAG	GAG	GTG	GTG	CGC	1349
	Val	Glu	Ile	Pro	Ala	Val	Phe	Asp	Glu	Ala	His	Gln	Glu	Val	Val	Arg	
		210				215						220					
	TGG	TTC	CGC	GAG	GAC	CTT	GCG	GAC	GGC	CTG	CGG	ATC	GAC	CAC	CCG	GAC	1397
	Trp	Phe	Arg	Glu	Asp	Leu	Ala	Asp	Gly	Leu	Arg	Ile	Asp	His	Pro	Asp	
		225			230				235						240		
	GGC	CTC	GCT	GAC	CCC	GAG	GGG	TAC	CTG	AAG	CGA	CTC	CGG	GAA	GTC	ACC	1445
	Gly	Leu	Ala	Asp	Pro	Glu	Gly	Tyr	Leu	Lys	Arg	Leu	Arg	Glu	Val	Thr	
40				245					250					255			
	GGC	GGC	GCT	TAC	CTG	CTG	ATC	GAA	AAG	ATC	CTG	GAG	CCG	GGG	GAG	CAG	1493
	Gly	Gly	Ala	Tyr	Leu	Leu	Ile	Glu	Lys	Ile	Leu	Glu	Pro	Gly	Glu	Gln	
				260				265					270				
	CTG	CCC	GCC	AGC	TTC	GAG	TGT	GAA	GGC	ACC	ACA	GGC	TAC	GAC	GCC	CTC	1541
	Leu	Pro	Ala	Ser	Phe	Glu	Cys	Glu	Gly	Thr	Thr	Gly	Tyr	Asp	Ala	Leu	
			275				280					285					
45	GCC	GAC	GTC	GAC	CGG	GTT	CTC	GTG	GAC	CCG	CGC	GGC	CAG	GAA	CCG	CTG	1589
	Ala	Asp	Val	Asp	Arg	Val	Leu	Val	Asp	Pro	Arg	Gly	Gln	Glu	Pro	Leu	
		290				295						300					
	GAC	CGG	CTT	GAC	GCG	TCC	CTG	CGT	GGC	GGC	GAG	CCC	GCC	GAC	TAC	CAG	1637
	Asp	Arg	Leu	Asp	Ala	Ser	Leu	Arg	Gly	Gly	Glu	Pro	Ala	Asp	Tyr	Gln	
		305			310					315					320		
50	GAC	ATG	ATC	CGC	GGA	ACC	AAG	CGC	CGG	ATC	ACC	GAC	GGT	ATC	CTG	CAC	1685
	Asp	Met	Ile	Arg	Gly	Thr	Lys	Arg	Arg	Ile	Thr	Asp	Gly	Ile	Leu	His	
				325					330					335			
	TCG	GAG	ATC	CTG	CGG	CTG	GCC	CGG	CTG	GTT	CCG	GGC	GAC	GCC	AAC	GTT	1733
	Ser	Glu	Ile	Leu	Arg	Leu	Ala	Arg	Leu	Val	Pro	Gly	Asp	Ala	Asn	Val	
				340				345					350				

5	TCA	ATC	GAC	GCC	GGA	GCC	GAC	GCT	CTC	GCC	GAA	ATC	ATC	GCC	GCC	TTC	1781
	Ser	Ile	Asp	Ala	Gly	Ala	Asp	Ala	Leu	Ala	Glu	Ile	Ile	Ala	Ala	Phe	
	355							360						365			
	CCG	GTC	TAC	CGC	ACC	TAC	CTG	CCG	GAG	GGC	GCC	GAG	GTC	CTG	AAG	GAG	1829
	Pro	Val	Tyr	Arg	Thr	Tyr	Leu	Pro	Glu	Gly	Ala	Glu	Val	Leu	Lys	Glu	
	370						375					380					
10	GCG	TGC	GAG	CTT	GCC	GCG	CGT	AGG	CGG	CCG	GAA	CTC	GAC	CAG	GCC	ATC	1877
	Ala	Cys	Glu	Leu	Ala	Ala	Arg	Arg	Arg	Pro	Glu	Leu	Asp	Gln	Ala	Ile	
	385						390				395					400	
	CAG	GCT	CTG	CAG	CCG	CTG	CTG	GAC	ACG	GAC	CTC	GAG	CTT	GCC	CGG		1925
	Gln	Ala	Leu	Gln	Pro	Leu	Leu	Leu	Asp	Thr	Asp	Leu	Glu	Leu	Ala	Arg	
	405								410					415			
15	CGC	TTC	CAG	CAG	ACC	TCG	GGC	ATG	GTC	ATG	GCC	AAG	GGC	GTG	GAG	GAC	1973
	Arg	Phe	Gln	Gln	Thr	Ser	Gly	Met	Val	Met	Ala	Lys	Gly	Val	Glu	Asp	
	420							425						430			
	ACC	GCG	TTC	TTC	CGC	TAC	AAC	CGC	CTG	GGC	ACC	CTC	ACG	GAA	GTG	GGC	2021
	Thr	Ala	Phe	Phe	Arg	Tyr	Asn	Arg	Leu	Gly	Thr	Leu	Thr	Glu	Val	Gly	
	435						440					445					
20	GCC	GAC	CCC	ACC	GAG	TTC	GCC	GTG	GAG	CCG	GAC	GAG	TTC	CAC	GCC	CGG	2069
	Ala	Asp	Pro	Thr	Glu	Phe	Ala	Val	Glu	Pro	Asp	Glu	Phe	His	Ala	Arg	
	450						455					460					
	CTG	GCA	CGC	CGG	CAG	GCC	GAG	CTT	CCG	CTG	TCC	ATG	ACG	ACG	CTG	AGC	2117
	Leu	Ala	Arg	Arg	Gln	Ala	Glu	Leu	Pro	Leu	Ser	Met	Thr	Thr	Leu	Ser	
	465					470					475					480	
25	ACG	CAC	GAC	ACC	AAG	CGC	AGC	GAG	GAC	ACC	CGA	GCA	AGG	ATT	TCG	GTC	2165
	Thr	His	Asp	Thr	Lys	Arg	Ser	Glu	Asp	Thr	Arg	Ala	Arg	Ile	Ser	Val	
	485							490						495			
	ATT	TCC	GAG	GTT	GCG	GGT	GAC	TGG	GAA	AAG	GCC	TTG	AAC	CGG	CTG	CGC	2213
	Ile	Ser	Glu	Val	Ala	Gly	Asp	Trp	Glu	Lys	Ala	Leu	Asn	Arg	Leu	Arg	
	500							505					510				
30	GAC	CTG	GCC	CCG	CTG	CCG	GAC	GGC	CCG	CTG	TCC	GCG	CTG	CTC	TGG	CAG	2261
	Asp	Leu	Ala	Pro	Leu	Pro	Asp	Gly	Pro	Leu	Ser	Ala	Leu	Leu	Trp	Gln	
	515						520					525					
	GCC	ATT	GCC	GGC	GCC	TGG	CCC	AGC	CGG	GAA	CGC	CTG	CAG	TAC	TAC		2309
	Ala	Ile	Ala	Gly	Ala	Trp	Pro	Ala	Ser	Arg	Glu	Arg	Leu	Gln	Tyr	Tyr	
	530						535					540					
35	GCG	CTG	AAG	GCC	GCG	CGT	GAA	GCG	GGG	AAC	TCG	ACC	AAC	TGG	ACC	GAT	2357
	Ala	Leu	Lys	Ala	Ala	Arg	Glu	Ala	Gly	Asn	Ser	Thr	Asn	Trp	Thr	Asp	
	545					550				555						560	
	CCG	GCC	CCC	GCG	TTC	GAG	GAG	AAG	CTG	AAG	GCC	GCG	GTC	GAC	GCC	GTG	2405
	Pro	Ala	Pro	Ala	Phe	Glu	Glu	Lys	Leu	Lys	Ala	Ala	Val	Asp	Ala	Val	
	565							570					575				
40	TTC	GAC	AAT	CCC	GCC	GTG	CAG	GCC	GAG	GTG	GAA	GCC	CTC	GTC	GAG	CTC	2453
	Phe	Asp	Asn	Pro	Ala	Val	Gln	Ala	Glu	Val	Glu	Ala	Leu	Val	Glu	Leu	
	580							585					590				
	CTG	GAG	CCG	TAC	GGA	GCT	TCG	AAC	TCC	CTC	GCC	GCC	AAG	CTC	GTG	CAG	2501
	Leu	Glu	Pro	Tyr	Gly	Ala	Ser	Asn	Ser	Leu	Ala	Ala	Lys	Leu	Val	Gln	
	595						600					605					
45	CTG	ACC	ATG	CCC	GGC	GTC	CCG	GAC	GTC	TAC	CAG	GGC	ACG	GAG	TTC	TGG	2549
	Leu	Thr	Met	Pro	Gly	Val	Pro	Asp	Val	Tyr	Gln	Gly	Thr	Glu	Phe	Trp	
	610						615					620					
	GAC	CGG	TCG	CTG	ACG	GAC	CCG	GAC	AAC	CGG	CGG	CCG	TTC	AGC	TTC	GAC	2597
	Asp	Arg	Ser	Leu	Thr	Asp	Pro	Asp	Asn	Arg	Arg	Pro	Phe	Ser	Phe	Asp	
	625					630					635					640	
50	GAC	CGC	CGC	GCC	GCG	CTG	GAG	CAG	CTG	GAT	GCC	GGC	GAC	CTT	CCC	GCG	2645
	Asp	Arg	Arg	Ala	Ala	Leu	Glu	Gln	Leu	Asp	Ala	Gly	Asp	Leu	Pro	Ala	
	645						650						655				
	TCA	TTT	ACC	GAT	GAG	CGG	ACG	AAG	CTG	CTA	GTG	ACG	TCG	CGC	GCG	CTG	2693
	Ser	Phe	Thr	Asp	Glu	Arg	Thr	Lys	Leu	Leu	Val	Thr	Ser	Arg	Ala	Leu	
	660						665						670				
55	CGG	CTG	CGC	CGG	GAC	CGT	CCG	GAG	CTG	TTC	ACG	GGG	TAC	CGG	CCG	GTC	2741
	Arg	Leu	Arg	Arg	Asp	Arg	Pro	Glu	Leu	Phe	Thr	Gly	Tyr	Arg	Pro	Val	
	675						680						685				
	CTG	GCC	AGC	GGG	CCC	GCC	GCC	GGG	CAC	CTG	CTC	GCG	TTC	GAC	CGC	GGC	2789

5 Leu Ala Ser Gly Pro Ala Ala Gly His Leu Leu Ala Phe Asp Arg Gly
 690 695 700
 ACC GCG GCG GCG CCG GGT GCA TTG ACC CTC GCC ACG CGG CTT CCC TAC 2837
 Thr Ala Ala Ala Pro Gly Ala Leu Thr Leu Ala Thr Arg Leu Pro Tyr
 705 710 715 720
 GGG CTG GAA CAG TCG GGT GGA TGG CGG GAC ACC GCC GTC GAA CTT AAC 2885
 Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr Ala Val Glu Leu Asn
 725 730 735
 10 ACC GCC ATG AAA GAC GAA CTG ACC GGT GCC GGC TTC GGA CCG GGG GCA 2933
 Thr Ala Met Lys Asp Glu Leu Thr Gly Ala Gly Phe Gly Pro Gly Ala
 740 745 750
 GTG AAG ATC GCC GAC ATC TTC CGG TCG TTC CCC GTT GCG CTG CTG GTG 2981
 Val Lys Ile Ala Asp Ile Phe Arg Ser Phe Pro Val Ala Leu Leu Val
 755 760 765
 15 CCG CAG ACA GGA GGA GAG TCA 3002
 Pro Gln Thr Gly Gly Glu Ser
 770 775
 TGACGCACAC CTACCCGCGG GAAGCCGCGA AACCCGTCCT GGGCCCCGCA CGCTACGACG 3062
 TCTGGGCGCC C 3073

(13) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:20

(B) TYPE:amino acid

(D) TOPOLOGY:linear

(ii) MOLECULE TYPE:peptide

(v) FRAGMENT TYPE:N-terminal fragment

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:12:

Met Arg Thr Pro Ala Ser Thr Tyr Arg Leu Gln Ile Arg Arg Gly Phe Thr
 1 5 10 15
 30 Leu Phe Asp
 20

(14) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:20

(B) TYPE:amino acid

(D) TOPOLOGY:linear

(ii) MOLECULE TYPE:peptide

(v) FRAGMENT TYPE:N-terminal fragment

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:13:

Met Arg Thr Pro Val Ser Thr Tyr Arg Leu Gln Ile Arg Lys Gly Phe Thr
 1 5 10 15
 40 Leu Phe Asp
 20

(15) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS :

(A) LENGTH:21

(B) TYPE:amino acid

(D) TOPOLOGY:linear

(ii) MOLECULE TYPE:peptide

(v) FRAGMENT TYPE:internal fragment

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:14:

Arg Ser Glu Asp Thr Arg Ala Arg Ile Ser Val Ile Ala Glu Val Ala Pro
 1 5 10 15
 55 Glu Trp Glu Lys
 20

(16) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:21

(B) TYPE:amino acid

(D) TOPOLOGY:linear

(ii) MOLECULE TYPE:peptide

(v) FRAGMENT TYPE:internal fragment

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:15:

Leu Val Gln Leu Thr Met Pro Gly Val Pro Asp Val Tyr Gln Gly Thr Glu
 1 5 10 15
 Phe Trp Asp Arg
 20

(17) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:20

(B) TYPE:amino acid

(D) TOPOLOGY:linear

(ii) MOLECULE TYPE:peptide

(v) FRAGMENT TYPE:internal fragment

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:16:

Leu Val Gln Leu Thr Met Pro Gly Val Pro Asp Val Tyr Gln Gly Thr Glu
 1 5 10 15
 Phe Trp Asp
 20

(18) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:20

(B) TYPE:amino acid

(D) TOPOLOGY:linear

(ii) MOLECULE TYPE:peptide

(v) FRAGMENT TYPE:internal fragment

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:17:

Glu Gly Arg Gln Ser Arg Tyr Ala Glu Ala Phe Asp Val Asp Trp Asp Leu
 1 5 10 15
 Ala Gly Gly
 20

45 Claims

1. A DNA encoding an enzyme which forms a non-reducing saccharide having trehalose structure as an end unit from a reducing amylaceous saccharide having a degree of glucose polymerization of 3 or higher.
2. The DNA as claimed in claim 1, wherein said enzyme has the following physicochemical properties:
 - (1) Molecular weight
About 76,000-87,000 daltons on sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE); and
 - (2) Isoelectric point (pI)
About 3.6-4.6 on isoelectrophoresis.
3. The DNA as claimed in claim 1, wherein said enzyme has an amino acid sequence selected from the group consisting of those as shown in the following SEQ ID NOs:2 and 4 that initiate from the N-terminal, and

homologous amino acid sequences to the amino acid sequences:

5 SEQ ID NO:2
 Met Arg Thr Pro Ala Ser Thr Tyr Arg Leu Gln Ile Arg Arg Gly Phe Thr
 1 5 10 15
 10 Leu Phe Asp Ala Ala Glu Thr Val Pro Tyr Leu Lys Ser Leu Gly Val Asp
 20 25 30
 Trp Ile Tyr Leu Ser Pro Ile Leu Lys Ala Glu Ser Gly Ser Asp His Gly
 15 35 40 45 50
 Tyr Asp Val Thr Asp Pro Ala Val Val Asp Pro Glu Arg Gly Gly Pro Glu
 55 60 65
 20 Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Gly Ala Gly Met Gly Val Leu

25

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5 70 75 80 85
 Ile Asp Ile Val Pro Asn His Val Gly Val Ala Ser Pro Pro Gln Asn Pro
 90 95 100
 10 Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg Gly Ser Pro Tyr Ala Val Ala
 105 110 115
 15 Phe Asp Val Asp Trp Asp Leu Ala Gly Gly Arg Ile Arg Ile Pro Val Leu
 120 125 130 135
 Gly Ser Asp Asp Asp Leu Asp Gln Leu Glu Ile Lys Asp Gly Glu Leu Arg
 140 145 150
 20 Tyr Tyr Asp His Arg Phe Pro Leu Ala Glu Gly Ser Tyr Arg Asp Gly Asp
 155 160 165 170
 25 Ser Pro Gln Asp Val His Gly Arg Gln His Tyr Glu Leu Ile Gly Trp Arg
 175 180 185
 Arg Ala Asp Asn Glu Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu
 190 195 200
 30 Ala Gly Ile Arg Val Glu Val Pro Pro Val Phe Asp Glu Ala His Gln Glu
 205 210 215 220
 35 Val Val Arg Trp Phe Arg Ala Gly Leu Ala Asp Gly Leu Arg Ile Asp His
 225 230 235
 Pro Asp Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val
 240 245 250 255
 40 Thr Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln
 260 265 270
 45 Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu Ala
 275 280 285
 Asp Val Asp Arg Val Phe Val Asp Pro Arg Gly Gln Val Pro Leu Asp Arg
 290 295 300 305
 50 Leu Asp Ala Arg Leu Arg Gly Gly Ala Pro Ala Asp Tyr Glu Asp Met Ile
 310 315 320
 55

5 Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His Ser Glu Ile Leu
 325 330 335 340
 Arg Leu Ala Arg Leu Val Pro Glu Gln Thr Gly Ile Pro Gly Glu Ala Ala
 10 345 350 355
 Ala Asp Ala Ile Ala Glu Ile Ile Ala Ala Phe Pro Val Tyr Arg Ser Tyr
 360 365 370
 15 Leu Pro Glu Gly Ala Glu Ile Leu Lys Glu Ala Cys Asp Leu Ala Ala Arg
 375 380 385 390
 Arg Arg Pro Glu Leu Gly Gln Thr Val Gln Leu Leu Gln Pro Leu Leu Leu
 20 395 400 405
 Asp Thr Asp Leu Glu Ile Ser Arg Arg Phe Gln Gln Thr Ser Gly Met Val
 410 415 420 425
 25 Met Ala Lys Gly Val Glu Asp Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly
 430 435 440
 Thr Leu Thr Glu Val Gly Ala Asp Pro Thr Glu Phe Ser Leu Glu Pro Glu
 30 445 450 455
 Glu Phe His Val Arg Met Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met
 460 465 470 475
 35 Thr Thr Leu Ser Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg
 480 485 490
 Ile Ser Val Ile Ala Glu Val Ala Pro Glu Trp Glu Lys Ala Leu Asp Arg
 40 495 500 505 510
 Leu Asn Thr Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Thr Leu Leu Trp
 45 515 520 525
 Gln Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Ser Tyr
 530 535 540
 50 Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Ser Trp Thr Asp Pro
 545 550 555 560
 Asp Pro Ala Phe Glu Glu Ala Leu Ser Ala Val Val Asp Ser Ala Phe Asp

5 565 570 575
 Asn Pro Glu Val Arg Ala Glu Leu Glu Ala Leu Val Gly Leu Leu Ala Pro
 580 585 590 595
 10 His Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln Leu Thr Met Pro
 600 605 610
 Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp Asp Arg Ser Leu Thr
 15 615 620 625
 Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Ala Glu Arg Ile Arg Ala Leu
 630 635 640 645
 20 Asp Gln Leu Asp Ala Gly His Arg Pro Asp Ser Phe Gln Asp Glu Ala Val
 650 655 660
 Lys Leu Leu Val Thr Ser Arg Ala Leu Arg Leu Arg Arg Asn Arg Pro Glu
 25 665 670 675 680
 Leu Phe Thr Gly Tyr Arg Pro Val His Ala Arg Gly Pro Ala Ala Gly His
 685 690 695
 30 Leu Val Ala Phe Asp Arg Gly Ala Gly Gly Val Leu Ala Leu Ala Thr Arg
 700 705 710
 Leu Pro Tyr Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr Ala Val Glu
 35 715 720 725 730
 Leu Glu Ala Ala Met Thr Asp Glu Leu Thr Gly Ser Thr Phe Gly Pro Gly
 735 740 745
 40 Pro Ala Ala Leu Ser Glu Val Phe Arg Ala Tyr Pro Val Ala Leu Leu Val
 750 755 760 765
 Pro Ala Thr Gly Gly Lys Ser
 45 770

 50

 55

SEQ ID NO:4

Met Arg Thr Pro Val Ser Thr Tyr Arg Leu Gln Ile Arg Lys Gly Phe Thr
 1 5 10 15

5 Leu Phe Asp Ala Ala Lys Thr Val Pro Tyr Leu His Ser Leu Gly Val Asp
 20 25 30
 Trp Val Tyr Leu Ser Pro Val Leu Thr Ala Glu Gln Gly Ser Asp His Gly
 10 35 40 45 50
 Tyr Asp Val Thr Asp Pro Ser Ala Val Asp Pro Glu Arg Gly Gly Pro Glu
 55 60 65
 15 Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Ala Ala Gly Met Gly Val Leu
 70 75 80 85
 Ile Asp Ile Val Pro Asn His Val Gly Val Ala Thr Pro Ala Gln Asn Pro
 20 90 95 100
 Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg Gln Ser Arg Tyr Ala Glu Ala
 105 110 115
 25 Phe Asp Val Asp Trp Asp Leu Ala Gly Gly Arg Ile Arg Leu Pro Val Leu
 120 125 130 135
 Gly Ser Asp Asp Asp Leu Asp Gln Leu Glu Ile Arg Asp Gly Glu Leu Arg
 30 140 145 150
 Tyr Tyr Asp His Arg Phe Pro Leu Ala Glu Gly Thr Tyr Ala Glu Gly Asp
 155 160 165 170
 35 Ala Pro Arg Asp Val His Ala Arg Gln His Tyr Glu Leu Ile Gly Trp Arg
 175 180 185
 Arg Ala Asp Asn Glu Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu
 40 190 195 200
 Ala Gly Val Arg Val Glu Ile Pro Ala Val Phe Asp Glu Ala His Gln Glu
 205 210 215 220
 45 Val Val Arg Trp Phe Arg Glu Asp Leu Ala Asp Gly Leu Arg Ile Asp His
 225 230 235
 Pro Asp Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val
 50 240 245 250 255
 Thr Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln
 55

5 260 265 270
 Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu Ala
 275 280 285
 10 Asp Val Asp Arg Val Leu Val Asp Pro Arg Gly Gln Glu Pro Leu Asp Arg
 290 295 300 305
 Leu Asp Ala Ser Leu Arg Gly Gly Glu Pro Ala Asp Tyr Gln Asp Met Ile
 15 310 315 320
 Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His Ser Glu Ile Leu
 325 330 335 340
 20 Arg Leu Ala Arg Leu Val Pro Gly Asp Ala Asn Val Ser Ile Asp Ala Gly
 345 350 355
 Ala Asp Ala Leu Ala Glu Ile Ile Ala Ala Phe Pro Val Tyr Arg Thr Tyr
 25 360 365 370
 Leu Pro Glu Gly Ala Glu Val Leu Lys Glu Ala Cys Glu Leu Ala Ala Arg
 375 380 385 390
 30 Arg Arg Pro Glu Leu Asp Gln Ala Ile Gln Ala Leu Gln Pro Leu Leu Leu
 395 400 405
 Asp Thr Asp Leu Glu Leu Ala Arg Arg Phe Gln Gln Thr Ser Gly Met Val
 35 410 415 420 425
 Met Ala Lys Gly Val Glu Asp Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly
 430 435 440
 40 Thr Leu Thr Glu Val Gly Ala Asp Pro Thr Glu Phe Ala Val Glu Pro Asp
 445 450 455
 Glu Phe His Ala Arg Leu Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met
 45 460 465 470 475
 Thr Thr Leu Ser Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg
 480 485 490
 50 Ile Ser Val Ile Ser Glu Val Ala Gly Asp Trp Glu Lys Ala Leu Asn Arg
 495 500 505 510
 55

5 Leu Arg Asp Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Ala Leu Leu Trp
 515 520 525
 10 Gln Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Tyr Tyr
 530 535 540
 15 Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Asn Trp Thr Asp Pro
 545 550 555 560
 20 Ala Pro Ala Phe Glu Glu Lys Leu Lys Ala Ala Val Asp Ala Val Phe Asp
 565 570 575
 25 Asn Pro Ala Val Gln Ala Glu Val Glu Ala Leu Val Glu Leu Leu Glu Pro
 580 585 590 595
 30 Tyr Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln Leu Thr Met Pro
 600 605 610
 35 Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp Asp Arg Ser Leu Thr
 615 620 625
 40 Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Asp Asp Arg Arg Ala Ala Leu
 630 635 640 645
 45 Glu Gln Leu Asp Ala Gly Asp Leu Pro Ala Ser Phe Thr Asp Glu Arg Thr
 650 655 660
 50 Lys Leu Leu Val Thr Ser Arg Ala Leu Arg Leu Arg Arg Asp Arg Pro Glu
 665 670 675 680
 55 Leu Phe Thr Gly Tyr Arg Pro Val Leu Ala Ser Gly Pro Ala Ala Gly His
 685 690 695
 60 Leu Leu Ala Phe Asp Arg Gly Thr Ala Ala Ala Pro Gly Ala Leu Thr Leu
 700 705 710
 65 Ala Thr Arg Leu Pro Tyr Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr
 715 720 725 730
 70 Ala Val Glu Leu Asn Thr Ala Met Lys Asp Glu Leu Thr Gly Ala Gly Phe
 735 740 745
 75 Gly Pro Gly Ala Val Lys Ile Ala Asp Ile Phe Arg Ser Phe Pro Val Ala

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Leu Leu Val Pro Gln Thr Gly Gly Glu Ser

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4. The DNA as claimed in claim 1, which has a base sequence selected from the group consisting of those as shown in the following SEQ ID NOs:1 and 3 that initiate from the 5'-terminus, homologous base sequences to the base sequences, and complementary base sequences to these base sequences:

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SEQ ID NO:1

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ATGAGGACAC CCGCCTCGAC CTACCGGCTG CAGATCAGGC GGGGTTTCAC GCTGTTTGAT 60
 GCCGCCGAGA CCGTGCCCTA CCTGAAGTCA CTCGGGGTGG ACTGGATCTA CCTGTCGCCCC 120
 ATCCTGAAGG CAGAGAGCGG CTCCGACCAC GGCTATGACG TCACCGATCC CGCCGTAGTG 180
 GACCCGAGC GCGGCGGCCC TGAAGGGCTG GCCGCGGTGT CCAAGGCGGC CCGCGGTGCC 240
 GGCATGGGCG TGCTGATCGA CATCGTGCCG AACCACGTGG GCGTGGCGTC GCCGCCGAG 300
 AACCCGTGGT GGTGGTCGCT GCTCAAGGAA GGGCGGGGT CGCCCTACGC CGTGGCGTTC 360
 GACGTCGACT GGGACCTGGC GGGGGGCCGC ATCCGGATCC CCGTCCTGGG CAGCGACGAC 420
 GATCTGGACC AGCTCGAAAT CAAGGACGGC GAGCTGCGGT ACTACGACCA CCGCTTCCCG 480
 CTGGCCGAGG GCAGCTACCG GGACGGCGAC TCCCCGAGG ACGTCCACGG CCGGCAGCAC 540
 TACGAACTCA TCGGCTGGCG GCGCGCCGAC AATGAACTGA ACTACCGCCG GTTCTTCGCG 600
 GTGAACACGC TCGCCGGCAT CCGGGTGGAG GTGCCGCCGG TCTTCGATGA AGCGCACCAG 660
 GAGGTGGTGC GCTGGTTCCG TCGGGGGCTC GCCGACGGGC TGCGGATCGA CCACCCGGAC 720
 GGCCTGGCCG ATCCCGAGGG GTATTTGAAG CGGCTCCGTG AGGTCACCGG GGGCGCGTAC 780
 CTGCTCATCG AAAAGATCCT CGAGCCGGGC GAACAGTTGC CGGCCAGCTT CGAGTGCGAA 840
 GGCACCACCG GCTACGACGC CCTCGCGGAT GTCGACAGGG TCTTCGTGGA CCCGCGGGGA 900
 CAGGTGCCGC TGGACCGTCT GGACGCACGG CTGCGCGGCG GTGCGCCGGC CGACTACGAG 960
 GACATGATCC GCGGGACCAA GCGCCGGATC ACCGACGGCA TCCTGCACTC CGAGATCCTG 1020
 CGCCTTGCCA GGCTGGTGCC CGAGCAGACC GGAATTCCCG GGGAGGCGGC CGCGGATGCG 1080
 ATCGCGGAGA TCATCGCGGC CTTCCCGGTC TACCGGTCCT ATCTTCCCGA GGGCGCGGAG 1140
 ATCCTGAAGG AGGCCTGCGA CCTCGCCGCG CGGAGGCGTC CGGAACTGGG CCAGACCGTC 1200

5 CAGCTGCTGC AGCCGCTGCT GCTGGATACC GACCTCGAGA TTTCCCGCAG GTTCCAGCAG 1260
ACCTCGGGAA TGGTCATGGC CAAAGGCGTG GAGGACACCG CGTTCTTCCG CTACAACCGG 1320
CTGGGAACGC TCACCGAGGT GGGCGCCGAC CCCACCGAGT TCTCGCTGGA ACCGGAGGAG 1380
10 TTTACGTCC GGATGGCCCC CCGGCAGGCC GAACTCCCGC TCTCCATGAC CACCCTGAGC 1440
ACGCACGACA CCAAGCGCAG CGAGGACACC CGGGCCCGGA TCTCGGTGAT CGCCGAGGTC 1500
GCGCCTGAAT GGGAAAAGGC CCTGGACAGG CTGAACACCC TCGCTCCGCT GCCGGACGGC 1560
15 CCGCTCTCCA CGCTGCTCTG GCAGGCGATT GCGGGGGCAT GGCCGGCCAG CCGGGAACGC 1620
CTTCAGTCCT ACGCCCTGAA AGCGGCGCGC GAAGCCGGGA ACTCGACCAG CTGGACCGAT 1680
CCGGACCCCG CATTCGAGGA GGCACCTTCC GCCGTCGTCG ACTCCGCCTT CGACAATCCG 1740
20 GAGGTGCGTG CGGAACTTGA GGCCCTGGTG GGCCTCCTTG CGCCGCACGG TGCCTCCAAC 1800
TCGCTCGCGG CAAAGCTTGT CCAGCTGACC ATGCCGGGCG TTCCGGACGT GTACCAGGGC 1860
ACCGAGTTCT GGGACAGGTC GCTGACCGAT CCGGACAACC GCGCCCCCTT CAGCTTCGCC 1920
25 GAACGGATTA GGGCCTTGGA CCAGTTGGAC GCCGGCCACC GTCCGGACTC CTTCCAGGAC 1980
GAGGCGGTCA AGCTGCTGGT CACCTCGAGG GCGCTGCGGC TCGGCGGAA CCGGCCCGAG 2040
CTCTTCACCG GCTACCGCCC CGTGCATGCC AGGGGCCCCG CCGCCGGGCA CCTGGTGGCG 2100
30 TTCGACCGCG GCGCCGGGGG AGTGCTGGCG CTTGCCACCC GGCTCCCCTA CGGGCTGGAA 2160
CAGTCGGGCG GCTGGCGGGA CACCGCCGTC GAGCTTGAAG CCGCCATGAC GGACGAACTG 2220
ACCGGCTCCA CTTTCGGGCC GGGACCGGCG GCGCTGTCAG AAGTCTTCCG GGCCTACCCG 2280
35 GTGGCCTTGT TGGTCCCCGC GACAGGAGGC AAGTCA 2316

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SEQ ID NO:3

5 ATGAGAACGC CAGTCTCCAC GTACAGGCTG CAGATCAGGA AGGGATTCAC ACTCTTCGAC 60
GCGGCCAAAA CCGTTCCGTA CCTGCACTCG CTCGGCGTCG ACTGGGTCTA CCTTTCTCCG 120
GTCCTGACTG CCGAGCAGGG CTCCGACCAC GGGTACGACG TCACCGATCC CTCCGCCGTC 180
10 GACCCCGAAC GCGGCGGGCC GGAGGGCCTC GCGGCGGTTT CCAAGGCGGC CCGCGCCGCG 240
GGCATGGGCG TGCTGATCGA CATCGTGCCC AACCACGTGG GCGTCGCGAC GCCGGCGCAG 300
AACCCCTGGT GGTGGTCGCT GCTCAAGGAG GGACGCCAGT CCCGTTACGC GGAGGCGTTC 360
15 GACGTCGATT GGGACCTCGC CGGGGGACGC ATCCGGCTGC CGGTGCTCGG CAGCGACGAT 420
GACCTCGACC AGCTCGAAAT CAGGGACGGG GAGCTGCGGT ACTACGACCA CCGATTCCCG 480

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5 CTCGCCGAGG GAACCTACGC CGAAGGCGAC GCCCCGCGGG ATGTCCACGC CCGGCAGCAC 540
 TACGAGCTCA TCGGCTGGCG CCGCGCGGAC AACGAGCTGA ACTACCGCCG CTTTTTCGCG 600
 GTGAACACGC TCGCCGGCGT CCGCGTGGA ATCCCCGCCG TCTTCGACGA GGCACACCAG 660
 10 GAGGTGGTGC GCTGGTTCCG CGAGGACCTT GCGGACGGCC TCGGGATCGA CCACCCGGAC 720
 GGCCTCGCTG ACCCCGAGGG GTACCTGAAG CGACTCCGGG AAGTCACCGG CGGCGCTTAC 780
 CTGCTGATCG AAAAGATCCT GGAGCCGGGG GAGCAGCTGC CCGCCAGCTT CGAGTGTGAA 840
 15 GGCACCACAG GCTACGACGC CCTCGCCGAC GTCGACCGGG TTCTCGTGGA CCCGCGCGGC 900
 CAGGAACCGC TGGACCGGCT TGACGCGTCC CTGCGTGGCG GCGAGCCCGC CGACTACCAG 960
 GACATGATCC GCGGAACCA GCGCCGGATC ACCGACGGTA TCCTGCACTC GGAGATCCTG 1020
 20 CGGCTGGCCC GGCTGGTTCC GGGCGACGCC AACGTTTCAA TCGACGCCGG AGCCGACGCT 1080
 CTCGCCGAAA TCATCGCCGC CTTCCCGGTC TACCGCACCT ACCTGCCGGA GGGCGCCGAG 1140
 GTCCTGAAGG AGGCGTGCGA GCTTGCCGCG CGTAGGCGGC CGGAACTCGA CCAGGCCATC 1200
 25 CAGGCTCTGC AGCCGCTGCT GCTGGACACG GACCTCGAGC TTGCCCGGCG CTTCCAGCAG 1260
 ACCTCGGGCA TGGTCATGGC CAAGGGCGTG GAGGACACCG CGTTCTTCCG CTACAACCGC 1320
 CTGGGCACCC TCACGGAAGT GGGCGCCGAC CCCACCGAGT TCGCCGTGGA GCCGGACGAG 1380
 30 TTCCACGCCC GGCTGGCAGC CCGGCAGGCC GAGCTTCCGC TGTCCATGAC GACGCTGAGC 1440
 ACGCACGACA CCAAGCGCAG CGAGGACACC CGAGCAAGGA TTTCGGTCAT TTCCGAGGTT 1500
 GCGGGTGACT GGGAAAAGGC CTTGAACCGG CTGCGCGACC TGGCCCCGCT GCCGGACGGC 1560
 35 CCGCTGTCCG CGCTGCTCTG GCAGGCCATT GCCGGCGCCT GGCCCGCCAG CCGGGAACGC 1620
 CTGCAGTACT ACGCGCTGAA GGCCGCGCGT GAAGCGGGGA ACTCGACCAA CTGGACCGAT 1680
 CCGGCCCCCG CGTTCGAGGA GAAGCTGAAG GCCGCGGTCTG ACGCCGTGTT CGACAATCCC 1740
 40 GCCGTGCAGG CCGAGGTGGA AGCCCTCGTC GAGCTCCTGG AGCCGTACGG AGCTTCGAAC 1800
 TCCCTCGCCG CCAAGCTCGT GCAGCTGACC ATGCCCGGCG TCCCGGACGT CTACCAGGGC 1860
 ACGGAGTTCT GGGACCGGTC GCTGACGGAC CCGGACAACC GGCGGCCGTT CAGCTTCGAC 1920
 45 GACCGCCGCG CCGCGCTGGA GCAGCTGGAT GCCGGCGACC TTCCCGCGTC ATTTACCGAT 1980
 GAGCGGACGA AGCTGCTAGT GACGTCGCGC GCGCTGCGGC TCGCCGGGA CCGTCCGGAG 2040
 CTGTTACAGG GGTACCGGCC GGTCTGGCC AGCGGGCCCG CCGCCGGGCA CCTGCTCGCG 2100
 50 TTGACCGCG GCACCGCGGC GCGCCGGGT GCATTGACCC TCGCCACGCG GCTTCCCTAC 2160
 GGGCTGGAAC AGTCGGGTGG ATGGCGGGAC ACCGCCGTCTG AACTTAACAC CGCCATGAAA 2220

GACGAACTGA CCGGTGCCGG CTTCCGACCG GGGGCAGTGA AGATCGCCGA CATCTTCCGG 2280
 TCGTTCCCCG TTGCGCTGCT GGTGCCGCAG ACAGGAGGAG AGTCA 2325

5. The DNA as claimed in claim 4, wherein one or more bases in SEQ ID NO:1 or 3 are replaced with other bases by means of degeneracy of genetic code without alternating the amino acid sequence of the following SEQ ID NO:2 or 4:

SEQ ID NO:2

Met Arg Thr Pro Ala Ser Thr Tyr Arg Leu Gln Ile Arg Arg Gly Phe Thr
 1 5 10 15
 Leu Phe Asp Ala Ala Glu Thr Val Pro Tyr Leu Lys Ser Leu Gly Val Asp
 20 25 30
 Trp Ile Tyr Leu Ser Pro Ile Leu Lys Ala Glu Ser Gly Ser Asp His Gly
 35 40 45 50
 Tyr Asp Val Thr Asp Pro Ala Val Val Asp Pro Glu Arg Gly Gly Pro Glu
 55 60 65
 Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Gly Ala Gly Met Gly Val Leu
 70 75 80 85
 Ile Asp Ile Val Pro Asn His Val Gly Val Ala Ser Pro Pro Gln Asn Pro
 90 95 100
 Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg Gly Ser Pro Tyr Ala Val Ala
 105 110 115
 Phe Asp Val Asp Trp Asp Leu Ala Gly Gly Arg Ile Arg Ile Pro Val Leu
 120 125 130 135
 Gly Ser Asp Asp Asp Leu Asp Gln Leu Glu Ile Lys Asp Gly Glu Leu Arg
 140 145 150
 Tyr Tyr Asp His Arg Phe Pro Leu Ala Glu Gly Ser Tyr Arg Asp Gly Asp
 155 160 165 170
 Ser Pro Gln Asp Val His Gly Arg Gln His Tyr Glu Leu Ile Gly Trp Arg
 175 180 185

5 Arg Ala Asp Asn Glu Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu
 190 195 200
 Ala Gly Ile Arg Val Glu Val Pro Pro Val Phe Asp Glu Ala His Gln Glu
 10 205 210 215 220
 Val Val Arg Trp Phe Arg Ala Gly Leu Ala Asp Gly Leu Arg Ile Asp His
 225 230 235
 15 Pro Asp Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val
 240 245 250 255
 Thr Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln
 20 260 265 270
 Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu Ala
 275 280 285
 25 Asp Val Asp Arg Val Phe Val Asp Pro Arg Gly Gln Val Pro Leu Asp Arg
 290 295 300 305
 Leu Asp Ala Arg Leu Arg Gly Gly Ala Pro Ala Asp Tyr Glu Asp Met Ile
 30 310 315 320
 Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His Ser Glu Ile Leu
 325 330 335 340
 35 Arg Leu Ala Arg Leu Val Pro Glu Gln Thr Gly Ile Pro Gly Glu Ala Ala
 345 350 355
 Ala Asp Ala Ile Ala Glu Ile Ile Ala Ala Phe Pro Val Tyr Arg Ser Tyr
 40 360 365 370
 Leu Pro Glu Gly Ala Glu Ile Leu Lys Glu Ala Cys Asp Leu Ala Ala Arg
 375 380 385 390
 45 Arg Arg Pro Glu Leu Gly Gln Thr Val Gln Leu Leu Gln Pro Leu Leu Leu
 395 400 405
 Asp Thr Asp Leu Glu Ile Ser Arg Arg Phe Gln Gln Thr Ser Gly Met Val
 50 410 415 420 425
 Met Ala Lys Gly Val Glu Asp Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly

5 430 435 440
 Thr Leu Thr Glu Val Gly Ala Asp Pro Thr Glu Phe Ser Leu Glu Pro Glu
 445 450 455
 10 Glu Phe His Val Arg Met Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met
 460 465 470 475
 Thr Thr Leu Ser Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg
 15 480 485 490
 Ile Ser Val Ile Ala Glu Val Ala Pro Glu Trp Glu Lys Ala Leu Asp Arg
 495 500 505 510
 20 Leu Asn Thr Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Thr Leu Leu Trp
 515 520 525
 Gln Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Ser Tyr
 25 530 535 540
 Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Ser Trp Thr Asp Pro
 545 550 555 560
 30 Asp Pro Ala Phe Glu Glu Ala Leu Ser Ala Val Val Asp Ser Ala Phe Asp
 565 570 575
 Asn Pro Glu Val Arg Ala Glu Leu Glu Ala Leu Val Gly Leu Leu Ala Pro
 35 580 585 590 595
 His Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln Leu Thr Met Pro
 600 605 610
 40 Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp Asp Arg Ser Leu Thr
 615 620 625
 Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Ala Glu Arg Ile Arg Ala Leu
 45 630 635 640 645
 Asp Gln Leu Asp Ala Gly His Arg Pro Asp Ser Phe Gln Asp Glu Ala Val
 50 650 655 660
 Lys Leu Leu Val Thr Ser Arg Ala Leu Arg Leu Arg Arg Asn Arg Pro Glu
 665 670 675 680
 55

5 Leu Phe Thr Gly Tyr Arg Pro Val His Ala Arg Gly Pro Ala Ala Gly His
 685 690 695
 Leu Val Ala Phe Asp Arg Gly Ala Gly Gly Val Leu Ala Leu Ala Thr Arg
 700 705 710
 10 Leu Pro Tyr Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr Ala Val Glu
 715 720 725 730
 Leu Glu Ala Ala Met Thr Asp Glu Leu Thr Gly Ser Thr Phe Gly Pro Gly
 15 735 740 745
 Pro Ala Ala Leu Ser Glu Val Phe Arg Ala Tyr Pro Val Ala Leu Leu Val
 750 755 760 765
 20 Pro Ala Thr Gly Gly Lys Ser
 770

25

30 SEQ ID NO:4
 Met Arg Thr Pro Val Ser Thr Tyr Arg Leu Gln Ile Arg Lys Gly Phe Thr
 1 5 10 15
 35 Leu Phe Asp Ala Ala Lys Thr Val Pro Tyr Leu His Ser Leu Gly Val Asp
 20 25 30
 Trp Val Tyr Leu Ser Pro Val Leu Thr Ala Glu Gln Gly Ser Asp His Gly
 40 35 40 45 50
 Tyr Asp Val Thr Asp Pro Ser Ala Val Asp Pro Glu Arg Gly Gly Pro Glu
 55 60 65
 45 Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Ala Ala Gly Met Gly Val Leu
 70 75 80 85
 Ile Asp Ile Val Pro Asn His Val Gly Val Ala Thr Pro Ala Gln Asn Pro
 50 90 95 100
 Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg Gln Ser Arg Tyr Ala Glu Ala
 105 110 115
 55 Phe Asp Val Asp Trp Asp Leu Ala Gly Gly Arg Ile Arg Leu Pro Val Leu

5	120	125	130	135
	Gly Ser Asp Asp Asp Leu Asp Gln Leu Glu Ile Arg Asp Gly Glu Leu Arg			
	140	145	150	
10	Tyr Tyr Asp His Arg Phe Pro Leu Ala Glu Gly Thr Tyr Ala Glu Gly Asp			
	155	160	165	170
	Ala Pro Arg Asp Val His Ala Arg Gln His Tyr Glu Leu Ile Gly Trp Arg			
15	175	180	185	
	Arg Ala Asp Asn Glu Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu			
	190	195	200	
20	Ala Gly Val Arg Val Glu Ile Pro Ala Val Phe Asp Glu Ala His Gln Glu			
	205	210	215	220
	Val Val Arg Trp Phe Arg Glu Asp Leu Ala Asp Gly Leu Arg Ile Asp His			
25	225	230	235	
	Pro Asp Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val			
	240	245	250	255
30	Thr Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln			
	260	265	270	
	Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu Ala			
35	275	280	285	
	Asp Val Asp Arg Val Leu Val Asp Pro Arg Gly Gln Glu Pro Leu Asp Arg			
	290	295	300	305
40	Leu Asp Ala Ser Leu Arg Gly Gly Glu Pro Ala Asp Tyr Gln Asp Met Ile			
	310	315	320	
45	Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His Ser Glu Ile Leu			
	325	330	335	340
	Arg Leu Ala Arg Leu Val Pro Gly Asp Ala Asn Val Ser Ile Asp Ala Gly			
50	345	350	355	
	Ala Asp Ala Leu Ala Glu Ile Ile Ala Ala Phe Pro Val Tyr Arg Thr Tyr			
	360	365	370	

5 Leu Pro Glu Gly Ala Glu Val Leu Lys Glu Ala Cys Glu Leu Ala Ala Arg
 375 380 385 390
 Arg Arg Pro Glu Leu Asp Gln Ala Ile Gln Ala Leu Gln Pro Leu Leu Leu
 10 395 400 405
 Asp Thr Asp Leu Glu Leu Ala Arg Arg Phe Gln Gln Thr Ser Gly Met Val
 410 415 420 425
 15 Met Ala Lys Gly Val Glu Asp Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly
 430 435 440
 Thr Leu Thr Glu Val Gly Ala Asp Pro Thr Glu Phe Ala Val Glu Pro Asp
 20 445 450 455
 Glu Phe His Ala Arg Leu Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met
 460 465 470 475
 25 Thr Thr Leu Ser Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg
 480 485 490
 Ile Ser Val Ile Ser Glu Val Ala Gly Asp Trp Glu Lys Ala Leu Asn Arg
 30 495 500 505 510
 Leu Arg Asp Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Ala Leu Leu Trp
 515 520 525
 35 Gln Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Tyr Tyr
 530 535 540
 Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Asn Trp Thr Asp Pro
 40 545 550 555 560
 Ala Pro Ala Phe Glu Glu Lys Leu Lys Ala Ala Val Asp Ala Val Phe Asp
 565 570 575
 45 Asn Pro Ala Val Gln Ala Glu Val Glu Ala Leu Val Glu Leu Leu Glu Pro
 580 585 590 595
 Tyr Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln Leu Thr Met Pro
 50 600 605 610
 Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp Asp Arg Ser Leu Thr
 55

5 615 620 625
 Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Asp Asp Arg Arg Ala Ala Leu
 630 635 640 645
 10 Glu Gln Leu Asp Ala Gly Asp Leu Pro Ala Ser Phe Thr Asp Glu Arg Thr
 650 655 660
 Lys Leu Leu Val Thr Ser Arg Ala Leu Arg Leu Arg Arg Asp Arg Pro Glu
 15 665 670 675 680
 Leu Phe Thr Gly Tyr Arg Pro Val Leu Ala Ser Gly Pro Ala Ala Gly His
 685 690 695
 20 Leu Leu Ala Phe Asp Arg Gly Thr Ala Ala Ala Pro Gly Ala Leu Thr Leu
 700 705 710
 Ala Thr Arg Leu Pro Tyr Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr
 25 715 720 725 730
 Ala Val Glu Leu Asn Thr Ala Met Lys Asp Glu Leu Thr Gly Ala Gly Phe
 735 740 745
 30 Gly Pro Gly Ala Val Lys Ile Ala Asp Ile Phe Arg Ser Phe Pro Val Ala
 750 755 760 765
 Leu Leu Val Pro Gln Thr Gly Gly Glu Ser
 35 770 775

40 6. The DNA as claimed in claim 1, which has the base sequence as shown in the following SEQ ID NO:10 or 11:

45 SEQ ID NO:10:

CGTGCTCTAC TTCAACGCGC ACGACGGCGA CGTCGTGTTC AAGCTCCCGT CGGATGAATA 60
 CGCCCCGGCC TGGGACGTCA TCATCGACAC CGCCGGCGCG GGTGCCGATT CCGAACCCGT 120
 50 GCAGGCTGGC GGCAAACTCA CCGTGGCAGC GAAATCGCTC GTGGTGCTCC GTGCCCACAG 180
 CGCCCCGGAG GAGGAACCGG ACCACTCGGT GGCCGCCCTCC CTCGCAGCGC TGACGCAGAC 240
 TGGCACC GCC GAAACCGCGG CGCTCACC GC CCCCACCGTT CCGGAGCCGA GGAAGACCAA 300
 55 GAAGGCAGCG CCGAAGCCGG AAGAGGAGGC TCCCGACGAG GCGGCGCCGA AGCCGGAAGA 360
 GAAGGCTCCC GACGAGGCGG CGGCGAAGCC GGAAGAGGCT GCTTCCGACG AGGCGGCGGC 420

5 GAAGCCGGAA GAGAAGGCTC CCGACGAGGC GGC GGCGAAG CCGGAAGAGG CTGCTTCCGA 480
 CGAGGCGGCG GCGAAGCCCG CGGGGAAGGC AGCGGCCAAA ACGGCCGGCA GGCGAGCGCC 540
 AGGCAAGCAG GGCGGGACGG GCTC 564
 10 ATG AGG ACA CCC GCC TCG ACC TAC CGG CTG CAG ATC AGG CGG GGT TTC 612
 Met Arg Thr Pro Ala Ser Thr Tyr Arg Leu Gln Ile Arg Arg Gly Phe
 1 5 10 15
 15 ACG CTG TTT GAT GCC GCC GAG ACC GTG CCC TAC CTG AAG TCA CTC GGG 660
 Thr Leu Phe Asp Ala Ala Glu Thr Val Pro Tyr Leu Lys Ser Leu Gly
 20 25 30
 20 GTG GAC TGG ATC TAC CTG TCG CCC ATC CTG AAG GCA GAG AGC GGC TCC 708
 Val Asp Trp Ile Tyr Leu Ser Pro Ile Leu Lys Ala Glu Ser Gly Ser
 35 40 45
 25 GAC CAC GGC TAT GAC GTC ACC GAT CCC GCC GTA GTG GAC CCG GAG CGC 756
 Asp His Gly Tyr Asp Val Thr Asp Pro Ala Val Val Asp Pro Glu Arg
 50 55 60
 30 GGC GGC CCT GAA GGG CTG GCC GCG GTG TCC AAG GCG GCC CGC GGT GCC 804
 Gly Gly Pro Glu Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Gly Ala
 65 70 75 80
 35 GGC ATG GGC GTG CTG ATC GAC ATC GTG CCG AAC CAC GTG GGC GTG GCG 852
 Gly Met Gly Val Leu Ile Asp Ile Val Pro Asn His Val Gly Val Ala
 85 90 95
 40 TCG CCG CCG CAG AAC CCG TGG TGG TGG TCG CTG CTC AAG GAA GGG CGC 900
 Ser Pro Pro Gln Asn Pro Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg
 100 105 110
 45 GGG TCG CCC TAC GCC GTG GCG TTC GAC GTC GAC TGG GAC CTG GCG GGG 948
 Gly Ser Pro Tyr Ala Val Ala Phe Asp Val Asp Trp Asp Leu Ala Gly
 115 120 125
 50 GGC CGC ATC CGG ATC CCC GTC CTG GGC AGC GAC GAC GAT CTG GAC CAG 996
 Gly Arg Ile Arg Ile Pro Val Leu Gly Ser Asp Asp Asp Leu Asp Gln
 55

5 130 135 140
 CTC GAA ATC AAG GAC GGC GAG CTG CGG TAC TAC GAC CAC CGC TTC CCG 1044
 Leu Glu Ile Lys Asp Gly Glu Leu Arg Tyr Tyr Asp His Arg Phe Pro
 10 145 150 155 160
 CTG GCC GAG GGC AGC TAC CGG GAC GGC GAC TCC CCG CAG GAC GTC CAC 1092
 Leu Ala Glu Gly Ser Tyr Arg Asp Gly Asp Ser Pro Gln Asp Val His
 15 165 170 175
 GGC CGG CAG CAC TAC GAA CTC ATC GGC TGG CGG CGC GCC GAC AAT GAA 1140
 Gly Arg Gln His Tyr Glu Leu Ile Gly Trp Arg Arg Ala Asp Asn Glu
 20 180 185 190
 CTG AAC TAC CGC CGG TTC TTC GCG GTG AAC ACG CTC GCC GGC ATC CGG 1188
 Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu Ala Gly Ile Arg
 25 195 200 205
 GTG GAG GTG CCG CCG GTC TTC GAT GAA GCG CAC CAG GAG GTG GTG CGC 1236
 Val Glu Val Pro Pro Val Phe Asp Glu Ala His Gln Glu Val Val Arg
 30 210 215 220
 TGG TTC CGT GCG GGG CTC GCC GAC GGG CTG CGG ATC GAC CAC CCG GAC 1284
 Trp Phe Arg Ala Gly Leu Ala Asp Gly Leu Arg Ile Asp His Pro Asp
 35 225 230 235 240
 GGC CTG GCC GAT CCC GAG GGG TAT TTG AAG CGG CTC CGT GAG GTC ACC 1332
 Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val Thr
 40 245 250 255
 GGG GGC GCG TAC CTG CTC ATC GAA AAG ATC CTC GAG CCG GGC GAA CAG 1380
 Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln
 45 260 265 270
 TTG CCG GCC AGC TTC GAG TGC GAA GGC ACC ACC GGC TAC GAC GCC CTC 1428
 Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu
 50 275 280 285
 GCG GAT GTC GAC AGG GTC TTC GTG GAC CCG CGG GGA CAG GTG CCG CTG 1476
 55

5 Ala Asp Val Asp Arg Val Phe Val Asp Pro Arg Gly Gln Val Pro Leu
 290 295 300
 GAC CGT CTG GAC GCA CGG CTG CGC GGC GGT GCG CCG GCC GAC TAC GAG 1524
 10 Asp Arg Leu Asp Ala Arg Leu Arg Gly Gly Ala Pro Ala Asp Tyr Glu
 305 310 315 320
 GAC ATG ATC CGC GGG ACC AAG CGC CGG ATC ACC GAC GGC ATC CTG CAC 1572
 15 Asp Met Ile Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His
 325 330 335
 TCC GAG ATC CTG CGC CTT GCC AGG CTG GTG CCC GAG CAG ACC GGA ATT 1620
 20 Ser Glu Ile Leu Arg Leu Ala Arg Leu Val Pro Glu Gln Thr Gly Ile
 340 345 350
 CCC GGG GAG GCG GCC GCG GAT GCG ATC GCG GAG ATC ATC GCG GCC TTC 1668
 25 Pro Gly Glu Ala Ala Ala Asp Ala Ile Ala Glu Ile Ile Ala Ala Phe
 355 360 365
 CCG GTC TAC CGG TCC TAT CTT CCC GAG GGC GCG GAG ATC CTG AAG GAG 1716
 30 Pro Val Tyr Arg Ser Tyr Leu Pro Glu Gly Ala Glu Ile Leu Lys Glu
 370 375 380
 GCC TGC GAC CTC GCC GCG CGG AGG CGT CCG GAA CTG GGC CAG ACC GTC 1764
 35 Ala Cys Asp Leu Ala Ala Arg Arg Arg Pro Glu Leu Gly Gln Thr Val
 385 390 395 400
 CAG CTG CTG CAG CCG CTG CTG CTG GAT ACC GAC CTC GAG ATT TCC CGC 1812
 40 Gln Leu Leu Gln Pro Leu Leu Leu Asp Thr Asp Leu Glu Ile Ser Arg
 405 410 415
 AGG TTC CAG CAG ACC TCG GGA ATG GTC ATG GCC AAA GGC GTG GAG GAC 1860
 45 Arg Phe Gln Gln Thr Ser Gly Met Val Met Ala Lys Gly Val Glu Asp
 420 425 430
 ACC GCG TTC TTC CGC TAC AAC CGG CTG GGA ACG CTC ACC GAG GTG GGC 1908
 50 Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly Thr Leu Thr Glu Val Gly
 435 440 445

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5 595 600 605
 CTG ACC ATG CCG GGC GTT CCG GAC GTG TAC CAG GGC ACC GAG TTC TGG 2436
 Leu Thr Met Pro Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp
 10 610 615 620
 GAC AGG TCG CTG ACC GAT CCG GAC AAC CGG CGC CCC TTC AGC TTC GCC 2484
 Asp Arg Ser Leu Thr Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Ala
 15 625 630 635 640
 GAA CGG ATT AGG GCC TTG GAC CAG TTG GAC GCC GGC CAC CGT CCG GAC 2532
 Glu Arg Ile Arg Ala Leu Asp Gln Leu Asp Ala Gly His Arg Pro Asp
 20 645 650 655
 TCC TTC CAG GAC GAG GCG GTC AAG CTG CTG GTC ACC TCG AGG GCG CTG 2580
 Ser Phe Gln Asp Glu Ala Val Lys Leu Leu Val Thr Ser Arg Ala Leu
 25 660 665 670
 CGG CTG CGG CGG AAC CGG CCC GAG CTC TTC ACC GGC TAC CGC CCC GTG 2628
 Arg Leu Arg Arg Asn Arg Pro Glu Leu Phe Thr Gly Tyr Arg Pro Val
 30 675 680 685
 CAT GCC AGG GGC CCC GCC GCC GGG CAC CTG GTG GCG TTC GAC CGC GGC 2676
 His Ala Arg Gly Pro Ala Ala Gly His Leu Val Ala Phe Asp Arg Gly
 35 690 695 700
 GCC GGG GGA GTG CTG GCG CTT GCC ACC CGG CTC CCC TAC GGG CTG GAA 2724
 Ala Gly Gly Val Leu Ala Leu Ala Thr Arg Leu Pro Tyr Gly Leu Glu
 40 705 710 715 720
 CAG TCG GGC GGC TGG CGG GAC ACC GCC GTC GAG CTT GAA GCC GCC ATG 2772
 Gln Ser Gly Gly Trp Arg Asp Thr Ala Val Glu Leu Glu Ala Ala Met
 45 725 730 735
 ACG GAC GAA CTG ACC GGC TCC ACT TTC GGG CCG GGA CCG GCG GCG CTG 2820
 Thr Asp Glu Leu Thr Gly Ser Thr Phe Gly Pro Gly Pro Ala Ala Leu
 50 740 745 750
 TCA GAA GTC TTC CGG GCC TAC CCG GTG GCC TTG TTG GTC CCC GCG ACA 2868

Ser Glu Val Phe Arg Ala Tyr Pro Val Ala Leu Leu Val Pro Ala Thr

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5

GGA GGC AAG TCA

2880

Gly Gly Lys Ser

770

10

TGACGCAGCC CAACGATGCG GCCAAGCCGG TGCAGGGAGC GGGGCGCTTC GATATC 2936

15

SEQ ID NO:11

20

GATCCGGACG GCAACCTCAT GTCCCCGGAG GACTGGGACA GCGGCTTCGG CCGTTCGGTG 60

GGCATGTTCC TCAACGGCGA CGGCATCCAG GGCCACGATG ACCGCGGCCG CCGCATCACG 120

GACGTGAAC TCTGCTGTA CTTCAACGCC CACGACGGCG ACGTCGAGTT CACGCTGCCG 180

25

CCGGACGAAT ACGCCCCGGC CTGGGACGTC ATCATCGACA CCGCCGGTGA AGGGGCCGAC 240

TCCAAGCCCG CGGACGCCGG AACCATCCTG TCCGTTGCGG CCAAGTCGCT GGTGTGCTT 300

CGCGCCCACA GCGCACCGGA GGAGGAGCCT GACCATTCCG TGGCTGCTTC CCTGGCTGCA 360

30

CTGACGCAGA CCGCCACCGC CGAGACGGCG GCGCTCACAG CTCCTGCCGT TCCCGAGCCG 420

GCCAAGACGA AGAAGCCGGC CGCTGACCCG GTTGCTGAAC CGGCCGACCC GCCGGTTCCT 480

35

GACCCGGCCG ACCCGGTTGC TGACCCGGTT GCTGACCCGG CGCCGGAACC GGCTGCGGAG 540

CCTGCGAAAT CCGCAGCGGA ACCTGGTGCG GAGCCTGCGA AGGACCCGGA GGAGCAGCCG 600

GCGGAAAAGC CGGCGCGCAA GCCTGCGGCA AAGCGCGGCG GCCACCTGAG GGCGGTCAAG 660

40

CCCGCTGGGG AGGACGC 677

ATG AGA ACG CCA GTC TCC ACG TAC AGG CTG CAG ATC AGG AAG GGA TTC 725

Met Arg Thr Pro Val Ser Thr Tyr Arg Leu Gln Ile Arg Lys Gly Phe

45

1 5 10 15

ACA CTC TTC GAC GCG GCC AAA ACC GTT CCG TAC CTG CAC TCG CTC GGC 773

Thr Leu Phe Asp Ala Ala Lys Thr Val Pro Tyr Leu His Ser Leu Gly

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20 25 30

GTC GAC TGG GTC TAC CTT TCT CCG GTC CTG ACT GCC GAG CAG GGC TCC 821

Val Asp Trp Val Tyr Leu Ser Pro Val Leu Thr Ala Glu Gln Gly Ser

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5 GAC CAC GGG TAC GAC GTC ACC GAT CCC TCC GCC GTC GAC CCC GAA CGC 869
 Asp His Gly Tyr Asp Val Thr Asp Pro Ser Ala Val Asp Pro Glu Arg
 50 55 60
 10 GGC GGG CCG GAG GGC CTC GCG GCG GTT TCC AAG GCG GCC CGC GCC GCG 917
 Gly Gly Pro Glu Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Ala Ala
 65 70 75 80
 15 GGC ATG GGC GTG CTG ATC GAC ATC GTG CCC AAC CAC GTG GGC GTC GCG 965
 Gly Met Gly Val Leu Ile Asp Ile Val Pro Asn His Val Gly Val Ala
 85 90 95
 20 ACG CCG GCG CAG AAC CCC TGG TGG TGG TCG CTG CTC AAG GAG GGA CGC 1013
 Thr Pro Ala Gln Asn Pro Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg
 100 105 110
 25 CAG TCC CGT TAC GCG GAG GCG TTC GAC GTC GAT TGG GAC CTC GCC GGG 1061
 Gln Ser Arg Tyr Ala Glu Ala Phe Asp Val Asp Trp Asp Leu Ala Gly
 115 120 125
 30 GGA CGC ATC CGG CTG CCG GTG CTC GGC AGC GAC GAT GAC CTC GAC CAG 1109
 Gly Arg Ile Arg Leu Pro Val Leu Gly Ser Asp Asp Asp Leu Asp Gln
 130 135 140
 35 CTC GAA ATC AGG GAC GGG GAG CTG CCG TAC TAC GAC CAC CGA TTC CCG 1157
 Leu Glu Ile Arg Asp Gly Glu Leu Arg Tyr Tyr Asp His Arg Phe Pro
 145 150 155 160
 40 CTC GCC GAG GGA ACC TAC GCC GAA GGC GAC GCC CCG CGG GAT GTC CAC 1205
 Leu Ala Glu Gly Thr Tyr Ala Glu Gly Asp Ala Pro Arg Asp Val His
 165 170 175
 45 GCC CGG CAG CAC TAC GAG CTC ATC GGC TGG CGC CGC GCG GAC AAC GAG 1253
 Ala Arg Gln His Tyr Glu Leu Ile Gly Trp Arg Arg Ala Asp Asn Glu
 180 185 190
 50 CTG AAC TAC CGC CGC TTT TTC GCG GTG AAC ACG CTC GCC GGC GTC CGC 1301
 Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu Ala Gly Val Arg
 55

5 195 200 205
 GTG GAA ATC CCC GCC GTC TTC GAC GAG GCA CAC CAG GAG GTG GTG CGC 1349
 Val Glu Ile Pro Ala Val Phe Asp Glu Ala His Gln Glu Val Val Arg
 10 210 215 220
 TGG TTC CGC GAG GAC CTT GCG GAC GGC CTG CGG ATC GAC CAC CCG GAC 1397
 Trp Phe Arg Glu Asp Leu Ala Asp Gly Leu Arg Ile Asp His Pro Asp
 15 225 230 235 240
 GGC CTC GCT GAC CCC GAG GGG TAC CTG AAG CGA CTC CGG GAA GTC ACC 1445
 Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val Thr
 20 245 250 255
 GGC GGC GCT TAC CTG CTG ATC GAA AAG ATC CTG GAG CCG GGG GAG CAG 1493
 Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln
 25 260 265 270
 CTG CCC GCC AGC TTC GAG TGT GAA GGC ACC ACA GGC TAC GAC GCC CTC 1541
 Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu
 30 275 280 285
 GCC GAC GTC GAC CGG GTT CTC GTG GAC CCG CGC GGC CAG GAA CCG CTG 1589
 Ala Asp Val Asp Arg Val Leu Val Asp Pro Arg Gly Gln Glu Pro Leu
 35 290 295 300
 GAC CGG CTT GAC GCG TCC CTG CGT GGC GGC GAG CCC GCC GAC TAC CAG 1637
 Asp Arg Leu Asp Ala Ser Leu Arg Gly Gly Glu Pro Ala Asp Tyr Gln
 40 305 310 315 320
 GAC ATG ATC CGC GGA ACC AAG CGC CGG ATC ACC GAC GGT ATC CTG CAC 1685
 Asp Met Ile Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His
 45 325 330 335
 TCG GAG ATC CTG CGG CTG GCC CGG CTG GTT CCG GGC GAC GCC AAC GTT 1733
 Ser Glu Ile Leu Arg Leu Ala Arg Leu Val Pro Gly Asp Ala Asn Val
 50 340 345 350
 TCA ATC GAC GCC GGA GCC GAC GCT CTC GCC GAA ATC ATC GCC GCC TTC 1781

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5 Ser Ile Asp Ala Gly Ala Asp Ala Leu Ala Glu Ile Ile Ala Ala Phe
 355 360 365
 CCG GTC TAC CGC ACC TAC CTG CCG GAG GGC GCC GAG GTC CTG AAG GAG 1829
 10 Pro Val Tyr Arg Thr Tyr Leu Pro Glu Gly Ala Glu Val Leu Lys Glu
 370 375 380
 GCG TGC GAG CTT GCC GCG CGT AGG CGG CCG GAA CTC GAC CAG GCC ATC 1877
 15 Ala Cys Glu Leu Ala Ala Arg Arg Arg Pro Glu Leu Asp Gln Ala Ile
 385 390 395 400
 CAG GCT CTG CAG CCG CTG CTG CTG GAC ACG GAC CTC GAG CTT GCC CGG 1925
 20 Gln Ala Leu Gln Pro Leu Leu Leu Asp Thr Asp Leu Glu Leu Ala Arg
 405 410 415
 CGC TTC CAG CAG ACC TCG GGC ATG GTC ATG GCC AAG GGC GTG GAG GAC 1973
 25 Arg Phe Gln Gln Thr Ser Gly Met Val Met Ala Lys Gly Val Glu Asp
 420 425 430
 ACC GCG TTC TTC CGC TAC AAC CGC CTG GGC ACC CTC ACG GAA GTG GGC 2021
 30 Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly Thr Leu Thr Glu Val Gly
 435 440 445
 GCC GAC CCC ACC GAG TTC GCC GTG GAG CCG GAC GAG TTC CAC GCC CGG 2069
 35 Ala Asp Pro Thr Glu Phe Ala Val Glu Pro Asp Glu Phe His Ala Arg
 450 455 460
 CTG GCA CGC CGG CAG GCC GAG CTT CCG CTG TCC ATG ACG ACG CTG AGC 2117
 40 Leu Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met Thr Thr Leu Ser
 465 470 475 480
 ACG CAC GAC ACC AAG CGC AGC GAG GAC ACC CGA GCA AGG ATT TCG GTC 2165
 45 Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg Ile Ser Val
 485 490 495
 ATT TCC GAG GTT GCG GGT GAC TGG GAA AAG GCC TTG AAC CGG CTG CGC 2213
 50 Ile Ser Glu Val Ala Gly Asp Trp Glu Lys Ala Leu Asn Arg Leu Arg
 500 505 510

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5 GAC CTG GCC CCG CTG CCG GAC GGC CCG CTG TCC GCG CTG CTC TGG CAG 2261
 Asp Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Ala Leu Leu Trp Gln
 515 520 525
 10 GCC ATT GCC GGC GCC TGG CCC GCC AGC CGG GAA CGC CTG CAG TAC TAC 2309
 Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Tyr Tyr
 530 535 540
 15 GCG CTG AAG GCC GCG CGT GAA GCG GGG AAC TCG ACC AAC TGG ACC GAT 2357
 Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Asn Trp Thr Asp
 545 550 555 560
 20 CCG GCC CCC GCG TTC GAG GAG AAG CTG AAG GCC GCG GTC GAC GCC GTG 2405
 Pro Ala Pro Ala Phe Glu Glu Lys Leu Lys Ala Ala Val Asp Ala Val
 565 570 575
 25 TTC GAC AAT CCC GCC GTG CAG GCC GAG GTG GAA GCC CTC GTC GAG CTC 2453
 Phe Asp Asn Pro Ala Val Gln Ala Glu Val Glu Ala Leu Val Glu Leu
 580 585 590
 30 CTG GAG CCG TAC GGA GCT TCG AAC TCC CTC GCC GCC AAG CTC GTG CAG 2501
 Leu Glu Pro Tyr Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln
 595 600 605
 35 CTG ACC ATG CCC GGC GTC CCG GAC GTC TAC CAG GGC ACG GAG TTC TGG 2549
 Leu Thr Met Pro Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp
 610 615 620
 40 GAC CGG TCG CTG ACG GAC CCG GAC AAC CGG CGG CCG TTC AGC TTC GAC 2597
 Asp Arg Ser Leu Thr Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Asp
 625 630 635 640
 45 GAC CGC CGC GCC GCG CTG GAG CAG CTG GAT GCC GGC GAC CTT CCC GCG 2645
 Asp Arg Arg Ala Ala Leu Glu Gln Leu Asp Ala Gly Asp Leu Pro Ala
 645 650 655
 50 TCA TTT ACC GAT GAG CGG ACG AAG CTG CTA GTG ACG TCG CGC GCG CTG 2693
 Ser Phe Thr Asp Glu Arg Thr Lys Leu Leu Val Thr Ser Arg Ala Leu
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5 660 665 670
 CGG CTG CGC CGG GAC CGT CCG GAG CTG TTC ACG GGG TAC CGG CCG GTC 2741
 Arg Leu Arg Arg Asp Arg Pro Glu Leu Phe Thr Gly Tyr Arg Pro Val
 10 675 680 685
 CTG GCC AGC GGG CCC GCC GCC GGG CAC CTG CTC GCG TTC GAC CGC GGC 2789
 Leu Ala Ser Gly Pro Ala Ala Gly His Leu Leu Ala Phe Asp Arg Gly
 15 690 695 700
 ACC GCG GCG GCG CCG GGT GCA TTG ACC CTC GCC ACG CGG CTT CCC TAC 2837
 Thr Ala Ala Ala Pro Gly Ala Leu Thr Leu Ala Thr Arg Leu Pro Tyr
 20 705 710 715 720
 GGG CTG GAA CAG TCG GGT GGA TGG CGG GAC ACC GCC GTC GAA CTT AAC 2885
 Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr Ala Val Glu Leu Asn
 25 725 730 735
 ACC GCC ATG AAA GAC GAA CTG ACC GGT GCC GGC TTC GGA CCG GGG GCA 2933
 Thr Ala Met Lys Asp Glu Leu Thr Gly Ala Gly Phe Gly Pro Gly Ala
 30 740 745 750
 GTG AAG ATC GCC GAC ATC TTC CGG TCG TTC CCC GTT GCG CTG CTG GTG 2981
 Val Lys Ile Ala Asp Ile Phe Arg Ser Phe Pro Val Ala Leu Leu Val
 35 755 760 765
 CCG CAG ACA GGA GGA GAG TCA 3002
 Pro Gln Thr Gly Gly Glu Ser
 40 770 775
 TGACGCACAC CTACCCGCGG GAAGCCGCGA AACCCGTCCT GGGCCCCGCA CGCTACGACG 3062
 TCTGGGCGCC C 3073
 45

- 50 7. The DNA as claimed in claim 1, which is derived from a microorganism selected from the group consisting of those of the genera *Rhizobium*, *Arthrobacter*, *Brevibacterium*, *Flavobacterium*, *Micrococcus*, *Curtobacterium*, *Mycobacterium* and *Terrabacter*.
- 55 8. A replicable recombinant DNA containing the DNA of claim 1 and a self-replicable vector.
9. The replicable recombinant DNA as claimed in claim 8, wherein said DNA encodes an enzyme having the following physicochemical properties:
 (1) Molecular weight

About 76,000-87,000 daltons on sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE); and

(2) Isoelectric point (pI)

About 3.6-4.6 on isoelectrophoresis.

10. The replicable recombinant DNA as claimed in claim 8, wherein said DNA encodes an enzyme having an amino acid sequence selected from the group consisting of those as shown in SEQ ID NOs:2 and 4 that initiate from the N-terminal, and homologous base sequences to these amino acid sequences:

SEQ ID NO:2

Met Arg Thr Pro Ala Ser Thr Tyr Arg Leu Gln Ile Arg Arg Gly Phe Thr
 1 5 10 15
 Leu Phe Asp Ala Ala Glu Thr Val Pro Tyr Leu Lys Ser Leu Gly Val Asp
 20 25 30
 Trp Ile Tyr Leu Ser Pro Ile Leu Lys Ala Glu Ser Gly Ser Asp His Gly
 35 40 45 50
 Tyr Asp Val Thr Asp Pro Ala Val Val Asp Pro Glu Arg Gly Gly Pro Glu
 25 55 60 65
 Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Gly Ala Gly Met Gly Val Leu
 30 70 75 80 85
 Ile Asp Ile Val Pro Asn His Val Gly Val Ala Ser Pro Pro Gln Asn Pro
 90 95 100

5 Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg Gly Ser Pro Tyr Ala Val Ala
 105 110 115
 Phe Asp Val Asp Trp Asp Leu Ala Gly Gly Arg Ile Arg Ile Pro Val Leu
 10 120 125 130 135
 Gly Ser Asp Asp Asp Leu Asp Gln Leu Glu Ile Lys Asp Gly Glu Leu Arg
 140 145 150
 15 Tyr Tyr Asp His Arg Phe Pro Leu Ala Glu Gly Ser Tyr Arg Asp Gly Asp
 155 160 165 170
 Ser Pro Gln Asp Val His Gly Arg Gln His Tyr Glu Leu Ile Gly Trp Arg
 20 175 180 185
 Arg Ala Asp Asn Glu Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu
 190 195 200
 25 Ala Gly Ile Arg Val Glu Val Pro Pro Val Phe Asp Glu Ala His Gln Glu
 205 210 215 220
 Val Val Arg Trp Phe Arg Ala Gly Leu Ala Asp Gly Leu Arg Ile Asp His
 30 225 230 235
 Pro Asp Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val
 240 245 250 255
 35 Thr Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln
 260 265 270
 Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu Ala
 40 275 280 285
 Asp Val Asp Arg Val Phe Val Asp Pro Arg Gly Gln Val Pro Leu Asp Arg
 290 295 300 305
 45 Leu Asp Ala Arg Leu Arg Gly Gly Ala Pro Ala Asp Tyr Glu Asp Met Ile
 310 315 320
 Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His Ser Glu Ile Leu
 50 325 330 335 340
 Arg Leu Ala Arg Leu Val Pro Glu Gln Thr Gly Ile Pro Gly Glu Ala Ala
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5 345 350 355
 Ala Asp Ala Ile Ala Glu Ile Ile Ala Ala Phe Pro Val Tyr Arg Ser Tyr
 360 365 370
 10 Leu Pro Glu Gly Ala Glu Ile Leu Lys Glu Ala Cys Asp Leu Ala Ala Arg
 375 380 385 390
 Arg Arg Pro Glu Leu Gly Gln Thr Val Gln Leu Leu Gln Pro Leu Leu Leu
 15 395 400 405
 Asp Thr Asp Leu Glu Ile Ser Arg Arg Phe Gln Gln Thr Ser Gly Met Val
 410 415 420 425
 20 Met Ala Lys Gly Val Glu Asp Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly
 430 435 440
 Thr Leu Thr Glu Val Gly Ala Asp Pro Thr Glu Phe Ser Leu Glu Pro Glu
 25 445 450 455
 Glu Phe His Val Arg Met Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met
 460 465 470 475
 30 Thr Thr Leu Ser Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg
 480 485 490
 Ile Ser Val Ile Ala Glu Val Ala Pro Glu Trp Glu Lys Ala Leu Asp Arg
 35 495 500 505 510
 Leu Asn Thr Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Thr Leu Leu Trp
 515 520 525
 40 Gln Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Ser Tyr
 530 535 540
 Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Ser Trp Thr Asp Pro
 45 545 550 555 560
 Asp Pro Ala Phe Glu Glu Ala Leu Ser Ala Val Val Asp Ser Ala Phe Asp
 565 570 575
 50 Asn Pro Glu Val Arg Ala Glu Leu Glu Ala Leu Val Gly Leu Leu Ala Pro
 580 585 590 595
 55

5 His Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln Leu Thr Met Pro
 600 605 610
 Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp Asp Arg Ser Leu Thr
 10 615 620 625
 Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Ala Glu Arg Ile Arg Ala Leu
 630 635 640 645
 15 Asp Gln Leu Asp Ala Gly His Arg Pro Asp Ser Phe Gln Asp Glu Ala Val
 650 655 660
 Lys Leu Leu Val Thr Ser Arg Ala Leu Arg Leu Arg Arg Asn Arg Pro Glu
 20 665 670 675 680
 Leu Phe Thr Gly Tyr Arg Pro Val His Ala Arg Gly Pro Ala Ala Gly His
 685 690 695
 25 Leu Val Ala Phe Asp Arg Gly Ala Gly Gly Val Leu Ala Leu Ala Thr Arg
 700 705 710
 Leu Pro Tyr Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr Ala Val Glu
 30 715 720 725 730
 Leu Glu Ala Ala Met Thr Asp Glu Leu Thr Gly Ser Thr Phe Gly Pro Gly
 735 740 745
 35 Pro Ala Ala Leu Ser Glu Val Phe Arg Ala Tyr Pro Val Ala Leu Leu Val
 750 755 760 765
 Pro Ala Thr Gly Gly Lys Ser
 40 770
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 50
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SEQ ID NO:4

5 Met Arg Thr Pro Val Ser Thr Tyr Arg Leu Gln Ile Arg Lys Gly Phe Thr
1 5 10 15
Leu Phe Asp Ala Ala Lys Thr Val Pro Tyr Leu His Ser Leu Gly Val Asp
10 20 25 30
Trp Val Tyr Leu Ser Pro Val Leu Thr Ala Glu Gln Gly Ser Asp His Gly

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5 35 40 45 50
 Tyr Asp Val Thr Asp Pro Ser Ala Val Asp Pro Glu Arg Gly Gly Pro Glu
 55 60 65
 10 Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Ala Ala Gly Met Gly Val Leu
 70 75 80 85
 Ile Asp Ile Val Pro Asn His Val Gly Val Ala Thr Pro Ala Gln Asn Pro
 15 90 95 100
 Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg Gln Ser Arg Tyr Ala Glu Ala
 105 110 115
 20 Phe Asp Val Asp Trp Asp Leu Ala Gly Gly Arg Ile Arg Leu Pro Val Leu
 120 125 130 135
 Gly Ser Asp Asp Asp Leu Asp Gln Leu Glu Ile Arg Asp Gly Glu Leu Arg
 25 140 145 150
 Tyr Tyr Asp His Arg Phe Pro Leu Ala Glu Gly Thr Tyr Ala Glu Gly Asp
 155 160 165 170
 30 Ala Pro Arg Asp Val His Ala Arg Gln His Tyr Glu Leu Ile Gly Trp Arg
 175 180 185
 Arg Ala Asp Asn Glu Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu
 35 190 195 200
 Ala Gly Val Arg Val Glu Ile Pro Ala Val Phe Asp Glu Ala His Gln Glu
 205 210 215 220
 40 Val Val Arg Trp Phe Arg Glu Asp Leu Ala Asp Gly Leu Arg Ile Asp His
 225 230 235
 Pro Asp Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val
 240 245 250 255
 Thr Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln
 260 265 270
 50 Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu Ala
 275 280 285
 55

5 Asp Val Asp Arg Val Leu Val Asp Pro Arg Gly Gln Glu Pro Leu Asp Arg
 290 295 300 305
 Leu Asp Ala Ser Leu Arg Gly Gly Glu Pro Ala Asp Tyr Gln Asp Met Ile
 10 310 315 320
 Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His Ser Glu Ile Leu
 325 330 335 340
 15 Arg Leu Ala Arg Leu Val Pro Gly Asp Ala Asn Val Ser Ile Asp Ala Gly
 345 350 355
 Ala Asp Ala Leu Ala Glu Ile Ile Ala Ala Phe Pro Val Tyr Arg Thr Tyr
 20 360 365 370
 Leu Pro Glu Gly Ala Glu Val Leu Lys Glu Ala Cys Glu Leu Ala Ala Arg
 375 380 385 390
 25 Arg Arg Pro Glu Leu Asp Gln Ala Ile Gln Ala Leu Gln Pro Leu Leu Leu
 395 400 405
 Asp Thr Asp Leu Glu Leu Ala Arg Arg Phe Gln Gln Thr Ser Gly Met Val
 30 410 415 420 425
 Met Ala Lys Gly Val Glu Asp Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly
 430 435 440
 35 Thr Leu Thr Glu Val Gly Ala Asp Pro Thr Glu Phe Ala Val Glu Pro Asp
 445 450 455
 Glu Phe His Ala Arg Leu Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met
 40 460 465 470 475
 Thr Thr Leu Ser Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg
 480 485 490
 45 Ile Ser Val Ile Ser Glu Val Ala Gly Asp Trp Glu Lys Ala Leu Asn Arg
 495 500 505 510
 Leu Arg Asp Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Ala Leu Leu Trp
 50 515 520 525
 Gln Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Tyr Tyr
 55

5 530 535 540
 Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Asn Trp Thr Asp Pro
 545 550 555 560
 10 Ala Pro Ala Phe Glu Glu Lys Leu Lys Ala Ala Val Asp Ala Val Phe Asp
 565 570 575
 Asn Pro Ala Val Gln Ala Glu Val Glu Ala Leu Val Glu Leu Leu Glu Pro
 15 580 585 590 595
 Tyr Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln Leu Thr Met Pro
 600 605 610
 20 Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp Asp Arg Ser Leu Thr
 615 620 625
 Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Asp Asp Arg Arg Ala Ala Leu
 25 630 635 640 645
 Glu Gln Leu Asp Ala Gly Asp Leu Pro Ala Ser Phe Thr Asp Glu Arg Thr
 650 655 660
 30 Lys Leu Leu Val Thr Ser Arg Ala Leu Arg Leu Arg Arg Asp Arg Pro Glu
 665 670 675 680
 Leu Phe Thr Gly Tyr Arg Pro Val Leu Ala Ser Gly Pro Ala Ala Gly His
 35 685 690 695
 Leu Leu Ala Phe Asp Arg Gly Thr Ala Ala Ala Pro Gly Ala Leu Thr Leu
 700 705 710
 40 Ala Thr Arg Leu Pro Tyr Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr
 715 720 725 730
 45 Ala Val Glu Leu Asn Thr Ala Met Lys Asp Glu Leu Thr Gly Ala Gly Phe
 735 740 745
 Gly Pro Gly Ala Val Lys Ile Ala Asp Ile Phe Arg Ser Phe Pro Val Ala
 50 750 755 760 765
 Leu Leu Val Pro Gln Thr Gly Gly Glu Ser
 770 775

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11. The replicable recombinant DNA as claimed in claim 8, wherein said DNA has a base sequence selected from the group consisting of those as shown in the following SEQ ID NOs:1 and 3 that initiate from the 5'-terminus, homologous base sequences to the base sequences, and complementary base sequences to these base sequences:

SEQ ID NO:1

10 ATGAGGACAC CCGCCTCGAC CTACCGGCTG CAGATCAGGC GGGGTTTCAC GCTGTTTGAT 60
 GCCGCCGAGA CCGTGCCCTA CCTGAAGTCA CTCGGGGTGG ACTGGATCTA CCTGTGCCCC 120
 15 ATCCTGAAGG CAGAGAGCGG CTCCGACCAC GGCTATGACG TCACCGATCC CGCCGTAGTG 180
 GACCCGGAGC GCGGCGGCCC TGAAGGGCTG GCCGCGGTGT CCAAGGCGGC CCGCGGTGCC 240
 GGCATGGGCG TGCTGATCGA CATCGTGCCG AACCACGTGG GCGTGCGCTC GCCGCCGCAG 300
 20 AACCCGTGGT GGTGGTCGCT GCTCAAGGAA GGGCGCGGGT CGCCCTACGC CGTGGCGTTC 360
 GACGTGCACT GGGACCTGGC GGGGGGCCGC ATCCGGATCC CCGTCCTGGG CAGCGACGAC 420
 GATCTGGACC AGCTCGAAAT CAAGGACGGC GAGCTGCGGT ACTACGACCA CCGCTTCCCG 480
 25 CTGGCCGAGG GCAGCTACCG GGACGGCGAC TCCCCGCAGG ACGTCCACGG CCGGCAGCAC 540
 TACGAAGTCA TCGGCTGGCG GCGCGCCGAC AATGAAGTGA ACTACGCCG GTTCTTCGCG 600
 GTGAACACGC TCGCCGGCAT CCGGGTGGAG GTGCCGCCGG TCTTCGATGA AGCGCACCAG 660
 30 GAGGTGGTGC GCTGGTTCG TCGGGGCTC GCCACGGGC TCGGATCGA CCACCCGGAC 720
 GGCCTGGCCG ATCCCGAGGG GTATTTGAAG CGGCTCCGTG AGGTCACCGG GGGCGCGTAC 780
 CTGCTCATCG AAAAGATCCT CGAGCCGGGC GAACAGTTGC CGGCCAGCTT CGAGTGCGAA 840
 35 GGCACCAACCG GCTACGACGC CCTCGCGGAT GTCGACAGGG TCTTCGTGGA CCCGCGGGGA 900
 CAGGTGCCGC TGGACCGTCT GGACGCACGG CTGCGCGGCG GTGCGCCGGC CGACTACGAG 960
 GACATGATCC GCGGGACCAA GCGCCGGATC ACCGACGGCA TCCTGCACTC CGAGATCCTG 1020
 40 CGCCTTGCCA GGCTGGTGCC CGAGCAGACC GGAATTCCCG GGGAGGCGGC CGCGGATGCG 1080
 ATCGCGGAGA TCATCGCGGC CTTCCCGGTC TACCGGTCCT ATCTTCCCGA GGGCGCGGAG 1140
 ATCCTGAAGG AGGCCTGCGA CCTCGCCGCG CGGAGGCGTC CGGAAGTGGG CCAGACCGTC 1200
 45 CAGCTGCTGC AGCCGCTGCT GCTGGATACC GACCTCGAGA TTTCCCGCAG GTTCCAGCAG 1260
 ACCTCGGGAA TGGTCATGGC CAAAGGCGTG GAGGACACCG CGTTCTTCCG CTACAACCGG 1320

CTGGGAACGC TCACCGAGGT GGGCGCCGAC CCCACCGAGT TCTCGCTGGA ACCGGAGGAG 1380
5 TTTACAGTCC GGATGGCCCG CCGGCAGGCC GAACTCCCGC TCTCCATGAC CACCCTGAGC 1440
ACGCACGACA CCAAGCGCAG CGAGGACACC CGGGCCCGGA TCTCGGTGAT CGCCGAGGTC 1500
GCGCCTGAAT GGGAAAAGGC CCTGGACAGG CTGAACACCC TCGCTCCGCT GCCGGACGGC 1560
10 CCGCTCTCCA CGCTGCTCTG GCAGGCGATT GCGGGGGCAT GGCCGGCCAG CCGGGAACGC 1620
CTTCAGTCCT ACGCCCTGAA AGCGGCGCGC GAAGCCGGGA ACTCGACCAG CTGGACCGAT 1680
CCGGACCCCG CATTCGAGGA GGCACCTTCC GCCGTCGTCG ACTCCGCCTT CGACAATCCG 1740
15 GAGGTGCGTG CGGAACCTGA GGCCCTGGTG GGCCTCCTTG CGCCGCACGG TCGTCCAAC 1800
TCGCTCGCGG CAAAGCTTGT CCAGCTGACC ATGCCGGGCG TTCCGGACGT GTACCAGGGC 1860
ACCGAGTTCT GGGACAGGTC GCTGACCGAT CCGGACAACC GCGCCCCCTT CAGCTTCGCC 1920
20 GAACGGATTA GGGCCTTGGA CCAGTTGGAC GCCGGCCACC GTCCGGACTC CTTCCAGGAC 1980
GAGGCGGTCA AGCTGCTGGT CACCTCGAGG GCGCTGCGGC TCGGGCGGAA CCGGCCCGAG 2040
CTCTTCACCG GCTACCGCCC CGTGATGCC AGGGGCCCCG CCGCCGGGCA CCTGGTGGCG 2100
25 TTCGACCGCG GCGCCGGGGG AGTGCTGGCG CTTGCCACCC GGCTCCCCTA CGGGCTGGAA 2160
CAGTCGGGCG GCTGGCGGGA CACCGCCGTC GAGCTTGAAG CCGCCATGAC GGACGAACTG 2220
ACCGGCTCCA CTTTCGGGCC GGGACCGGCG GCGCTGTCAG AAGTCTTCG GGCCTACCCG 2280
30 GTGGCCTTGT TGGTCCCCGC GACAGGAGGC AAGTCA 2316

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SEQ ID NO:3

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ATGAGAACGC CAGTCTCCAC GTACAGGCTG CAGATCAGGA AGGGATTAC ACTCTTCGAC 60
GCGGCCAAAA CCGTTCGGTA CCTGCACTCG CTCGGCGTCG ACTGGGTCTA CCTTTCTCCG 120
GTCCTGACTG CCGAGCAGGG CTCCGACCAC GGGTACGACG TCACCGATCC CTCCGCCGTC 180
GACCCCGAAC GCGGCGGGCC GGAGGGCCTC GCGGCGGTTT CCAAGGCGGC CCGCGCCGCG 240
GGCATGGGCG TGCTGATCGA CATCGTGCCC AACCACGTGG GCGTCGCGAC GCCGGCGCAG 300
AACCCCTGGT GGTGGTCGCT GCTCAAGGAG GGACGCCAGT CCCGTTACGC GGAGGCGTTC 360
GACGTCGATT GGGACCTCGC CGGGGGACGC ATCCGGCTGC CGGTGCTCGG CAGCGACGAT 420
GACCTCGACC AGCTCGAAAT CAGGGACGGG GAGCTGCGGT ACTACGACCA CCGATTCCCG 480
CTCGCCGAGG GAACCTACGC CGAAGGCGAC GCCCGCGGG ATGTCCACGC CCGGCAGCAC 540
TACGAGCTCA TCGGCTGGCG CCGCGCGGAC AACGAGCTGA ACTACGCCG CTTTTTCGCG 600

5 GTGAACACGC TCGCCGGCGT CCGCGTGGAA ATCCCCGCCG TCTTCGACGA GGCACACCAG 660
 GAGGTGGTGC GCTGGTTCCG CGAGGACCTT GCGGACGGCC TCGGATCGA CCACCCGGAC 720
 GGCCTCGCTG ACCCCGAGGG GTACCTGAAG CCACTCCGGG AAGTCACCGG CGGCGCTTAC 780
 10 CTGCTGATCG AAAAGATCCT GGAGCCGGGG GAGCAGCTGC CCGCCAGCTT CGAGTGTGAA 840
 GGCACCACAG GCTACGACGC CCTCGCCGAC GTCGACCGGG TTCTCGTGGG CCCGCGCGGC 900
 CAGGAACCGC TGGACCGGCT TGACCGCTCC CTGCGTGGCG GCGAGCCCGC CGACTACCAG 960
 15 GACATGATCC GCGGAACCAA GCGCCGGATC ACCGACGGTA TCCTGCACTC GGAGATCCTG 1020
 CGGCTGGCCC GGCTGGTTCC GGGCGACGCC AACGTTTCAA TCGACGCCGG AGCCGACGCT 1080
 CTCGCCGAAA TCATCGCCGC CTTCCCGGTC TACCGCACTT ACCTGCCGGA GGGCGCCGAG 1140
 20 GTCCTGAAGG AGGCGTGCGA GCTTGCCGCG CGTAGGCGGC CGGAAGTCGA CCAGGCCATC 1200
 CAGGCTCTGC AGCCGCTGCT GCTGGACACG GACCTCGAGC TTGCCCGGCG CTTCCAGCAG 1260
 ACCTCGGGCA TGGTCATGGC CAAGGGCGTG GAGGACACCG CGTTCTTCCG CTACAACCGC 1320
 25 CTGGGCACCC TCACGGAAGT GGGCGCCGAC CCCACCGAGT TCGCCGTGGA GCCGGACGAG 1380
 TTCCACGCCC GGCTGGCAGC CCGGCAGGCC GAGCTTCCGC TGTCCATGAC GACGCTGAGC 1440
 ACGCAGGACA CCAAGCGCAG CGAGGACACC CGAGCAAGGA TTTCGGTCAT TTCCGAGGTT 1500
 30 GCGGGTGACT GGGAAAAGGC CTTGAACCGG CTGCGCGACC TGGCCCCGCT GCCGGACGGC 1560
 CCGCTGTCCG CGCTGCTCTG GCAGGCCATT GCCGGCGCCT GGCCCGCCAG CCGGGAACGC 1620
 CTGCAGTACT ACGCGCTGAA GGCCGCGCGT GAAGCGGGGA ACTCGACCAA CTGGACCGAT 1680
 35 CCGGCCCCCG CGTTCGAGGA GAAGCTGAAG GCCGCGGTCG ACGCCGTGTT CGACAATCCC 1740
 GCCGTGCAGG CCGAGGTGGA AGCCCTCGTC GAGCTCCTGG AGCCGTACGG AGCTTCGAAC 1800
 TCCCTCGCCG CCAAGCTCGT GCAGCTGACC ATGCCCGGCG TCCCGGACGT CTACCAGGGC 1860
 40 ACGGAGTTCT GGGACCGGTC GCTGACGGAC CCGGACAACC GCGGCGCGTT CAGCTTCGAC 1920
 GACCGCCGCG CCGCGCTGGA GCAGCTGGAT GCCGGCGACC TTCCCGCGTC ATTTACCGAT 1980
 GAGCGGACGA AGCTGCTAGT GACGTCGCGC GCGCTGCGGC TCGCGCGGGA CCGTCCGGAG 2040
 45 CTGTTACGG GGTACCGGCC GGTCTGGCC AGCGGGCCCG CCGCCGGGCA CCTGCTCGCG 2100
 TTGACCGCG GCACCGCGGC GCGCCGGGT GCATTGACCC TCGCCACGCG GCTTCCCTAC 2160
 GGGCTGGAAC AGTCGGGTGG ATGGCGGGAC ACCGCCGTCG AACTTAACAC CGCCATGAAA 2220
 50 GACGAAGTGA CCGGTGCCCG CTTCCGACCG GGGGCACTGA AGATCGCCGA CATCTTCCGG 2280
 TCGTTCCCCG TTGCGCTGCT GGTGCCGCAG ACAGGAGGAG AGTCA 2325

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12. The replicable recombinant DNA as claimed in claim 11, wherein one or more bases in SEQ ID NOs:1 and 3 are replaced with other bases by means of degeneracy of genetic code without alternating their corresponding amino acid sequences of the following SEQ ID NOs:2 and 4 in this order:

SEQ ID NO:2

10 Met Arg Thr Pro Ala Ser Thr Tyr Arg Leu Gln Ile Arg Arg Gly Phe Thr
 1 5 10 15
 Leu Phe Asp Ala Ala Glu Thr Val Pro Tyr Leu Lys Ser Leu Gly Val Asp
 15 20 25 30
 Trp Ile Tyr Leu Ser Pro Ile Leu Lys Ala Glu Ser Gly Ser Asp His Gly
 35 40 45 50
 20 Tyr Asp Val Thr Asp Pro Ala Val Val Asp Pro Glu Arg Gly Gly Pro Glu
 55 60 65
 Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Gly Ala Gly Met Gly Val Leu
 25 70 75 80 85
 Ile Asp Ile Val Pro Asn His Val Gly Val Ala Ser Pro Pro Gln Asn Pro
 90 95 100
 30 Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg Gly Ser Pro Tyr Ala Val Ala
 105 110 115
 Phe Asp Val Asp Trp Asp Leu Ala Gly Gly Arg Ile Arg Ile Pro Val Leu
 35 120 125 130 135
 Gly Ser Asp Asp Asp Leu Asp Gln Leu Glu Ile Lys Asp Gly Glu Leu Arg
 140 145 150
 40 Tyr Tyr Asp His Arg Phe Pro Leu Ala Glu Gly Ser Tyr Arg Asp Gly Asp
 155 160 165 170
 45 Ser Pro Gln Asp Val His Gly Arg Gln His Tyr Glu Leu Ile Gly Trp Arg
 175 180 185
 Arg Ala Asp Asn Glu Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu

5 190 195 200
 Ala Gly Ile Arg Val Glu Val Pro Pro Val Phe Asp Glu Ala His Gln Glu
 205 210 215 220
 10 Val Val Arg Trp Phe Arg Ala Gly Leu Ala Asp Gly Leu Arg Ile Asp His
 225 230 235
 Pro Asp Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val
 15 240 245 250 255
 Thr Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln
 260 265 270
 20 Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu Ala
 275 280 285
 Asp Val Asp Arg Val Phe Val Asp Pro Arg Gly Gln Val Pro Leu Asp Arg
 25 290 295 300 305
 Leu Asp Ala Arg Leu Arg Gly Gly Ala Pro Ala Asp Tyr Glu Asp Met Ile
 310 315 320
 30 Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His Ser Glu Ile Leu
 325 330 335 340
 Arg Leu Ala Arg Leu Val Pro Glu Gln Thr Gly Ile Pro Gly Glu Ala Ala
 35 345 350 355
 Ala Asp Ala Ile Ala Glu Ile Ile Ala Ala Phe Pro Val Tyr Arg Ser Tyr
 360 365 370
 40 Leu Pro Glu Gly Ala Glu Ile Leu Lys Glu Ala Cys Asp Leu Ala Ala Arg
 375 380 385 390
 Arg Arg Pro Glu Leu Gly Gln Thr Val Gln Leu Leu Gln Pro Leu Leu Leu
 45 395 400 405
 Asp Thr Asp Leu Glu Ile Ser Arg Arg Phe Gln Gln Thr Ser Gly Met Val
 410 415 420 425
 50 Met Ala Lys Gly Val Glu Asp Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly
 430 435 440

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5 Thr Leu Thr Glu Val Gly Ala Asp Pro Thr Glu Phe Ser Leu Glu Pro Glu
 445 450 455
 Glu Phe His Val Arg Met Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met
 10 460 465 470 475
 Thr Thr Leu Ser Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg
 480 485 490
 15 Ile Ser Val Ile Ala Glu Val Ala Pro Glu Trp Glu Lys Ala Leu Asp Arg
 495 500 505 510
 Leu Asn Thr Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Thr Leu Leu Trp
 20 515 520 525
 Gln Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Ser Tyr
 530 535 540
 25 Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Ser Trp Thr Asp Pro
 545 550 555 560
 Asp Pro Ala Phe Glu Glu Ala Leu Ser Ala Val Val Asp Ser Ala Phe Asp
 30 565 570 575
 Asn Pro Glu Val Arg Ala Glu Leu Glu Ala Leu Val Gly Leu Leu Ala Pro
 580 585 590 595
 35 His Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln Leu Thr Met Pro
 600 605 610
 Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp Asp Arg Ser Leu Thr
 40 615 620 625
 Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Ala Glu Arg Ile Arg Ala Leu
 630 635 640 645
 45 Asp Gln Leu Asp Ala Gly His Arg Pro Asp Ser Phe Gln Asp Glu Ala Val
 650 655 660
 50 Lys Leu Leu Val Thr Ser Arg Ala Leu Arg Leu Arg Arg Asn Arg Pro Glu
 665 670 675 680
 Leu Phe Thr Gly Tyr Arg Pro Val His Ala Arg Gly Pro Ala Ala Gly His
 55

685 690 695
 5 Leu Val Ala Phe Asp Arg Gly Ala Gly Gly Val Leu Ala Leu Ala Thr Arg
 700 705 710
 Leu Pro Tyr Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr Ala Val Glu
 10 715 720 725 730
 Leu Glu Ala Ala Met Thr Asp Glu Leu Thr Gly Ser Thr Phe Gly Pro Gly
 735 740 745
 15 Pro Ala Ala Leu Ser Glu Val Phe Arg Ala Tyr Pro Val Ala Leu Leu Val
 750 755 760 765
 Pro Ala Thr Gly Gly Lys Ser
 20 770

SEQ ID NO:4

30 Met Arg Thr Pro Val Ser Thr Tyr Arg Leu Gln Ile Arg Lys Gly Phe Thr
 1 5 10 15
 Leu Phe Asp Ala Ala Lys Thr Val Pro Tyr Leu His Ser Leu Gly Val Asp
 35 20 25 30
 Trp Val Tyr Leu Ser Pro Val Leu Thr Ala Glu Gln Gly Ser Asp His Gly
 35 40 45 50
 40 Tyr Asp Val Thr Asp Pro Ser Ala Val Asp Pro Glu Arg Gly Gly Pro Glu
 55 60 65
 Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Ala Ala Gly Met Gly Val Leu
 45 70 75 80 85
 Ile Asp Ile Val Pro Asn His Val Gly Val Ala Thr Pro Ala Gln Asn Pro
 90 95 100
 50 Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg Gln Ser Arg Tyr Ala Glu Ala
 105 110 115
 Phe Asp Val Asp Trp Asp Leu Ala Gly Gly Arg Ile Arg Leu Pro Val Leu
 55 120 125 130 135

5 Gly Ser Asp Asp Asp Leu Asp Gln Leu Glu Ile Arg Asp Gly Glu Leu Arg
 140 145 150
 Tyr Tyr Asp His Arg Phe Pro Leu Ala Glu Gly Thr Tyr Ala Glu Gly Asp
 10 155 160 165 170
 Ala Pro Arg Asp Val His Ala Arg Gln His Tyr Glu Leu Ile Gly Trp Arg
 175 180 185
 15 Arg Ala Asp Asn Glu Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu
 190 195 200
 Ala Gly Val Arg Val Glu Ile Pro Ala Val Phe Asp Glu Ala His Gln Glu
 20 205 210 215 220
 Val Val Arg Trp Phe Arg Glu Asp Leu Ala Asp Gly Leu Arg Ile Asp His
 225 230 235
 25 Pro Asp Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val
 240 245 250 255
 Thr Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln
 30 260 265 270
 Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu Ala
 275 280 285
 35 Asp Val Asp Arg Val Leu Val Asp Pro Arg Gly Gln Glu Pro Leu Asp Arg
 290 295 300 305
 Leu Asp Ala Ser Leu Arg Gly Gly Glu Pro Ala Asp Tyr Gln Asp Met Ile
 40 310 315 320
 Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His Ser Glu Ile Leu
 325 330 335 340
 45 Arg Leu Ala Arg Leu Val Pro Gly Asp Ala Asn Val Ser Ile Asp Ala Gly
 345 350 355
 Ala Asp Ala Leu Ala Glu Ile Ile Ala Ala Phe Pro Val Tyr Arg Thr Tyr
 50 360 365 370
 Leu Pro Glu Gly Ala Glu Val Leu Lys Glu Ala Cys Glu Leu Ala Ala Arg
 55

	375	380	385	390
5	Arg Arg Pro Glu Leu Asp Gln Ala Ile Gln Ala Leu Gln Pro Leu Leu Leu			
	395	400	405	
10	Asp Thr Asp Leu Glu Leu Ala Arg Arg Phe Gln Gln Thr Ser Gly Met Val			
	410	415	420	425
15	Met Ala Lys Gly Val Glu Asp Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly			
	430	435	440	
20	Thr Leu Thr Glu Val Gly Ala Asp Pro Thr Glu Phe Ala Val Glu Pro Asp			
	445	450	455	
25	Glu Phe His Ala Arg Leu Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met			
	460	465	470	475
30	Thr Thr Leu Ser Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg			
	480	485	490	
35	Ile Ser Val Ile Ser Glu Val Ala Gly Asp Trp Glu Lys Ala Leu Asn Arg			
	495	500	505	510
40	Leu Arg Asp Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Ala Leu Leu Trp			
	515	520	525	
45	Gln Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Tyr Tyr			
	530	535	540	
50	Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Asn Trp Thr Asp Pro			
	545	550	555	560
55	Ala Pro Ala Phe Glu Glu Lys Leu Lys Ala Ala Val Asp Ala Val Phe Asp			
	565	570	575	
60	Asn Pro Ala Val Gln Ala Glu Val Glu Ala Leu Val Glu Leu Leu Glu Pro			
	580	585	590	595
65	Tyr Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln Leu Thr Met Pro			
	600	605	610	
70	Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp Asp Arg Ser Leu Thr			
	615	620	625	

5 Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Asp Asp Arg Arg Ala Ala Leu
 630 635 640 645
 Glu Gln Leu Asp Ala Gly Asp Leu Pro Ala Ser Phe Thr Asp Glu Arg Thr
 10 650 655 660
 Lys Leu Leu Val Thr Ser Arg Ala Leu Arg Leu Arg Arg Asp Arg Pro Glu
 665 670 675 680
 15 Leu Phe Thr Gly Tyr Arg Pro Val Leu Ala Ser Gly Pro Ala Ala Gly His
 685 690 695
 Leu Leu Ala Phe Asp Arg Gly Thr Ala Ala Ala Pro Gly Ala Leu Thr Leu
 20 700 705 710
 Ala Thr Arg Leu Pro Tyr Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr
 715 720 725 730
 25 Ala Val Glu Leu Asn Thr Ala Met Lys Asp Glu Leu Thr Gly Ala Gly Phe
 735 740 745
 Gly Pro Gly Ala Val Lys Ile Ala Asp Ile Phe Arg Ser Phe Pro Val Ala
 30 750 755 760 765
 Leu Leu Val Pro Gln Thr Gly Gly Glu Ser
 770 775

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 40 13. The replicable recombinant DNA as claimed in claim 8, which has a base sequence selected from the group consisting of those as shown in SEQ ID NO:10 and 11:

SEQ ID NO:10:

45 CGTGCTCTAC TTCAACGCGC ACGACGGCGA CGTCGTGTTC AAGCTCCCGT CGGATGAATA 60
 CGCCCCGGCC TGGGACGTCA TCATCGACAC CGCCGGCGCG GGTGCCGATT CCGAACCCGT 120
 GCAGGCTGGC GGCAAACCTCA CCGTGGCAGC GAAATCGCTC GTGGTGCTCC GTGCCACAG 180
 50 CGCCCCGGAG GAGGAACCGG ACCACTCGGT GGCCGCCTCC CTCGCAGCGC TGACGCAGAC 240
 TGCAGCCGCC GAAACCGCGG CGCTCACCGC CCCCACCGTT CCGGAGCCGA GGAAGACCAA 300
 GAAGGCAGCG CCGAAGCCGG AAGAGGAGGC TCCGACGAG GCGGCGCCGA AGCCGGAAGA 360
 55 GAAGGCTCCC GACGAGGCGG CGGCGAAGCC GGAAGAGGCT GCTTCCGACG AGGCGGCGGC 420

5 GAAGCCGGAA GAGAAGGCTC CCGACGAGGC GGCGGCGAAG CCGGAAGAGG CTGCTTCCGA 480
 CGAGGCGGCG GCGAAGCCCG CGGGGAAGGC AGCGGCCAAA ACGGCCGGCA GGCGAGCGCC 540
 AGGCAAGCAG GGCGGGACGG GCTC 564
 10 ATG AGG ACA CCC GCC TCG ACC TAC CGG CTG CAG ATC AGG CGG GGT TTC 612
 Met Arg Thr Pro Ala Ser Thr Tyr Arg Leu Gln Ile Arg Arg Gly Phe
 1 5 10 15
 15 ACG CTG TTT GAT GCC GCC GAG ACC GTG CCC TAC CTG AAG TCA CTC GGG 660
 Thr Leu Phe Asp Ala Ala Glu Thr Val Pro Tyr Leu Lys Ser Leu Gly
 20 25 30
 20 GTG GAC TGG ATC TAC CTG TCG CCC ATC CTG AAG GCA GAG AGC GGC TCC 708
 Val Asp Trp Ile Tyr Leu Ser Pro Ile Leu Lys Ala Glu Ser Gly Ser
 35 40 45
 25 GAC CAC GGC TAT GAC GTC ACC GAT CCC GCC GTA GTG GAC CCG GAG CGC 756
 Asp His Gly Tyr Asp Val Thr Asp Pro Ala Val Val Asp Pro Glu Arg
 50 55 60
 30 GGC GGC CCT GAA GGG CTG GCC GCG GTG TCC AAG GCG GCC CGC GGT GCC 804
 Gly Gly Pro Glu Gly Leu Ala Ala Val Ser Lys Ala Ala Arg_Gly Ala
 65 70 75 80
 35 GGC ATG GGC GTG CTG ATC GAC ATC GTG CCG AAC CAC GTG GGC GTG GCG 852
 Gly Met Gly Val Leu Ile Asp Ile Val Pro Asn His Val Gly Val Ala
 85 90 95
 40 TCG CCG CCG CAG AAC CCG TGG TGG TGG TCG CTG CTC AAG GAA GGG CGC 900
 Ser Pro Pro Gln Asn Pro Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg
 100 105 110
 45 GGG TCG CCC TAC GCC GTG GCG TTC GAC GTC GAC TGG GAC CTG GCG GGG 948
 Gly Ser Pro Tyr Ala Val Ala Phe Asp Val Asp Trp Asp Leu Ala Gly
 115 120 125
 50 GGC CGC ATC CGG ATC CCC GTC CTG GGC AGC GAC GAC GAT CTG GAC CAG 996
 Gly Arg Ile Arg Ile Pro Val Leu Gly Ser Asp Asp Asp Leu Asp Gln
 55

5 130 135 140
 CTC GAA ATC AAG GAC GGC GAG CTG CGG TAC TAC GAC CAC CGC TTC CCG 1044
 Leu Glu Ile Lys Asp Gly Glu Leu Arg Tyr Tyr Asp His Arg Phe Pro
 10 145 150 155 160
 CTG GCC GAG GGC AGC TAC CGG GAC GGC GAC TCC CCG CAG GAC GTC CAC 1092
 Leu Ala Glu Gly Ser Tyr Arg Asp Gly Asp Ser Pro Gln Asp Val His
 15 165 170 175
 GGC CGG CAG CAC TAC GAA CTC ATC GGC TGG CGG CGC GCC GAC AAT GAA 1140
 Gly Arg Gln His Tyr Glu Leu Ile Gly Trp Arg Arg Ala Asp Asn Glu
 20 180 185 190
 CTG AAC TAC CGC CGG TTC TTC GCG GTG AAC ACG CTC GCC GGC ATC CGG 1188
 Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu Ala Gly Ile Arg
 25 195 200 205
 GTG GAG GTG CCG CCG GTC TTC GAT GAA GCG CAC CAG GAG GTG GTG CGC 1236
 Val Glu Val Pro Pro Val Phe Asp Glu Ala His Gln Glu Val Val Arg
 30 210 215 220
 TGG TTC CGT GCG GGG CTC GCC GAC GGG CTG CGG ATC GAC CAC CCG GAC 1284
 Trp Phe Arg Ala Gly Leu Ala Asp Gly Leu Arg Ile Asp His Pro Asp
 35 225 230 235 240
 GGC CTG GCC GAT CCC GAG GGG TAT TTG AAG CGG CTC CGT GAG GTC ACC 1332
 Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val Thr
 40 245 250 255
 GGG GGC GCG TAC CTG CTC ATC GAA AAG ATC CTC GAG CCG GGC GAA CAG 1380
 Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln
 45 260 265 270
 TTG CCG GCC AGC TTC GAG TGC GAA GGC ACC ACC GGC TAC GAC GCC CTC 1428
 Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu
 50 275 280 285
 GCG GAT GTC GAC AGG GTC TTC GTG GAC CCG CGG GGA CAG GTG CCG CTG 1476

5 Ala Asp Val Asp Arg Val Phe Val Asp Pro Arg Gly Gln Val Pro Leu
 290 295 300
 GAC CGT CTG GAC GCA CGG CTG CGC GGC GGT GCG CCG GCC GAC TAC GAG 1524
 10 Asp Arg Leu Asp Ala Arg Leu Arg Gly Gly Ala Pro Ala Asp Tyr Glu
 305 310 315 320
 GAC ATG ATC CGC GGG ACC AAG CGC CGG ATC ACC GAC GGC ATC CTG CAC 1572
 15 Asp Met Ile Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His
 325 330 335
 TCC GAG ATC CTG CGC CTT GCC AGG CTG GTG CCC GAG CAG ACC GGA ATT 1620
 20 Ser Glu Ile Leu Arg Leu Ala Arg Leu Val Pro Glu Gln Thr Gly Ile
 340 345 350
 CCC GGG GAG GCG GCC GCG GAT GCG ATC GCG GAG ATC ATC GCG GCC TTC 1668
 25 Pro Gly Glu Ala Ala Ala Asp Ala Ile Ala Glu Ile Ile Ala Ala Phe
 355 360 365
 CCG GTC TAC CGG TCC TAT CTT CCC GAG GGC GCG GAG ATC CTG AAG GAG 1716
 30 Pro Val Tyr Arg Ser Tyr Leu Pro Glu Gly Ala Glu Ile Leu Lys Glu
 370 375 380
 GCC TGC GAC CTC GCC GCG CGG AGG CGT CCG GAA CTG GGC CAG ACC GTC 1764
 35 Ala Cys Asp Leu Ala Ala Arg Arg Arg Pro Glu Leu Gly Gln Thr Val
 385 390 395 400
 CAG CTG CTG CAG CCG CTG CTG CTG GAT ACC GAC CTC GAG ATT TCC CGC 1812
 40 Gln Leu Leu Gln Pro Leu Leu Leu Asp Thr Asp Leu Glu Ile Ser Arg
 405 410 415
 AGG TTC CAG CAG ACC TCG GGA ATG GTC ATG GCC AAA GGC GTG GAG GAC 1860
 45 Arg Phe Gln Gln Thr Ser Gly Met Val Met Ala Lys Gly Val Glu Asp
 420 425 430
 ACC GCG TTC TTC CGC TAC AAC CGG CTG GGA ACG CTC ACC GAG GTG GGC 1908
 50 Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly Thr Leu Thr Glu Val Gly
 435 440 445

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5 GCC GAC CCC ACC GAG TTC TCG CTG GAA CCG GAG GAG TTT CAC GTC CGG 1956
 Ala Asp Pro Thr Glu Phe Ser Leu Glu Pro Glu Glu Phe His Val Arg
 450 455 460

10 ATG GCC CGC CGG CAG GCC GAA CTC CCG CTC TCC ATG ACC ACC CTG AGC 2004
 Met Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met Thr Thr Leu Ser
 465 470 475 480

15 ACG CAC GAC ACC AAG CGC AGC GAG GAC ACC CGG GCC CGG ATC TCG GTG 2052
 Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg Ile Ser Val
 485 490 495

20 ATC GCC GAG GTC GCG CCT GAA TGG GAA AAG GCC CTG GAC AGG CTG AAC 2100
 Ile Ala Glu Val Ala Pro Glu Trp Glu Lys Ala Leu Asp Arg Leu Asn
 500 505 510

25 ACC CTC GCT CCG CTG CCG GAC GGC CCG CTC TCC ACG CTG CTC TGG CAG 2148
 Thr Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Thr Leu Leu Trp Gln
 515 520 525

30 GCG ATT GCG GGG GCA TGG CCG GCC AGC CGG GAA CGC CTT CAG TCC TAC 2196
 Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Ser Tyr
 530 535 540

35 GCC CTG AAA GCG GCG CGC GAA GCC GGG AAC TCG ACC AGC TGG ACC GAT 2244
 Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Ser Trp Thr Asp
 545 550 555 560

40 CCG GAC CCG GCA TTC GAG GAG GCA CTT TCC GCC GTC GTC GAC TCC GCC 2292
 Pro Asp Pro Ala Phe Glu Glu Ala Leu Ser Ala Val Val Asp Ser Ala
 565 570 575

45 TTC GAC AAT CCG GAG GTG CGT GCG GAA CTT GAG GCC CTG GTG GGC CTC 2340
 Phe Asp Asn Pro Glu Val Arg Ala Glu Leu Glu Ala Leu Val Gly Leu
 580 585 590

50 CTT GCG CCG CAC GGT GCG TCC AAC TCG CTC GCG GCA AAG CTT GTC CAG 2388
 Leu Ala Pro His Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln

55

5 595 600 605
 CTG ACC ATG CCG GGC GTT CCG GAC GTG TAC CAG GGC ACC GAG TTC TGG 2436
 Leu Thr Met Pro Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp
 10 610 615 620
 GAC AGG TCG CTG ACC GAT CCG GAC AAC CGG CGC CCC TTC AGC TTC GCC 2484
 Asp Arg Ser Leu Thr Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Ala
 15 625 630 635 640
 GAA CGG ATT AGG GCC TTG GAC CAG TTG GAC GCC GGC CAC CGT CCG GAC 2532
 Glu Arg Ile Arg Ala Leu Asp Gln Leu Asp Ala Gly His Arg Pro Asp
 20 645 650 655
 TCC TTC CAG GAC GAG GCG GTC AAG CTG CTG GTC ACC TCG AGG GCG CTG 2580
 Ser Phe Gln Asp Glu Ala Val Lys Leu Leu Val Thr Ser Arg Ala Leu
 25 660 665 670
 CGG CTG CGG CGG AAC CGG CCC GAG CTC TTC ACC GGC TAC CGC CCC GTG 2628
 Arg Leu Arg Arg Asn Arg Pro Glu Leu Phe Thr Gly Tyr Arg Pro Val
 30 675 680 685
 CAT GCC AGG GGC CCC GCC GCC GGG CAC CTG GTG GCG TTC GAC CGC GGC 2676
 His Ala Arg Gly Pro Ala Ala Gly His Leu Val Ala Phe Asp Arg Gly
 35 690 695 700
 GCC GGG GGA GTG CTG GCG CTT GCC ACC CGG CTC CCC TAC GGG CTG GAA 2724
 Ala Gly Gly Val Leu Ala Leu Ala Thr Arg Leu Pro Tyr Gly Leu Glu
 40 705 710 715 720
 CAG TCG GGC GGC TGG CGG GAC ACC GCC GTC GAG CTT GAA GCC GCC ATG 2772
 Gln Ser Gly Gly Trp Arg Asp Thr Ala Val Glu Leu Glu Ala Ala Met
 45 725 730 735
 ACG GAC GAA CTG ACC GGC TCC ACT TTC GGG CCG GGA CCG GCG GCG CTG 2820
 Thr Asp Glu Leu Thr Gly Ser Thr Phe Gly Pro Gly Pro Ala Ala Leu
 50 740 745 750
 TCA GAA GTC TTC CGG GCC TAC CCG GTG GCC TTG TTG GTC CCC GCG ACA 2868
 55

Ser Glu Val Phe Arg Ala Tyr Pro Val Ala Leu Leu Val Pro Ala Thr

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765

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GGA GGC AAG TCA

2880

Gly Gly Lys Ser

770

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TGACGCAGCC CAACGATGCG GCCAAGCCGG TGCAGGGAGC GGGGCGCTTC GATATC

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SEQ ID NO:11

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GATCCGGACG GCAACCTCAT GTCCCCGGAG GACTGGGACA GCGGCTTCGG CCGTTCGGTG 60
 GGCATGTTCC TCAACGGCGA CGGCATCCAG GGCCACGATG ACCGCGGCCG CCGCATCACG 120
 GACGTGAACT TCCTGCTGTA CTTCAACGCC CACGACGGCG ACGTCGAGTT CACGCTGCCG 180
 CCGGACGAAT ACGCCCCGGC CTGGGACGTC ATCATCGACA CCGCCGGTGA AGGGGCCGAC 240
 TCCAAGCCCG CGGACGCCGG AACCATCCTG TCCGTTGCGG CCAAGTCGCT GGTGTGCTT 300
 CGCGCCCACA GCGCACCGGA GGAGGAGCCT GACCATTCCG TGGCTGCTTC CCTGGCTGCA 360
 CTGACGCAGA CCGCCACCGC CGAGACGGCG GCGCTCACAG CTCCTGCCGT TCCCGAGCCG 420
 GCCAAGACGA AGAAGCCGGC CGCTGACCCG GTTGCTGAAC CGGCCGACCC GCCGGTTGCT 480
 GACCCGGCCG ACCCGGTTGC TGACCCGGTT GCTGACCCGG CGCCGGAACC GGCTGCGGAG 540
 CCTGCGAAAT CCGCAGCGGA ACCTGGTGCG GAGCCTGCGA AGGACCCGGA GGAGCAGCCG 600
 GCGGAAAAGC CGGCGCGCAA GCCTGCGGCA AAGCGCGGCG GCCACCTGAG GGCGGTCAAG 660
 CCCGCTGGGG AGGACGC 677
 ATG AGA ACG CCA GTC TCC ACG TAC AGG CTG CAG ATC AGG AAG GGA TTC 725
 Met Arg Thr Pro Val Ser Thr Tyr Arg Leu Gln Ile Arg Lys Gly Phe
 1 5 10 15
 ACA CTC TTC GAC GCG GCC AAA ACC GTT CCG TAC CTG CAC TCG CTC GGC 773
 Thr Leu Phe Asp Ala Ala Lys Thr Val Pro Tyr Leu His Ser Leu Gly
 20 25 30
 GTC GAC TGG GTC TAC CTT TCT CCG GTC CTG ACT GCC GAG CAG GGC TCC 821
 Val Asp Trp Val Tyr Leu Ser Pro Val Leu Thr Ala Glu Gln Gly Ser
 35 40 45

5 GAC CAC GGG TAC GAC GTC ACC GAT CCC TCC GCC GTC GAC CCC GAA CGC 869
 Asp His Gly Tyr Asp Val Thr Asp Pro Ser Ala Val Asp Pro Glu Arg
 50 55 60
 10 GGC GGG CCG GAG GGC CTC GCG GCG GTT TCC AAG GCG GCC CGC GCC GCG 917
 Gly Gly Pro Glu Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Ala Ala
 65 70 75 80
 15 GGC ATG GGC GTG CTG ATC GAC ATC GTG CCC AAC CAC GTG GGC GTC GCG 965
 Gly Met Gly Val Leu Ile Asp Ile Val Pro Asn His Val Gly Val Ala
 85 90 95
 20 ACG CCG GCG CAG AAC CCC TGG TGG TGG TCG CTG CTC AAG GAG GGA CGC 1013
 Thr Pro Ala Gln Asn Pro Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg
 100 105 110
 25 CAG TCC CGT TAC GCG GAG GCG TTC GAC GTC GAT TGG GAC CTC GCC GGG 1061
 Gln Ser Arg Tyr Ala Glu Ala Phe Asp Val Asp Trp Asp Leu Ala Gly
 115 120 125
 30 GGA CGC ATC CGG CTG CCG GTG CTC GGC AGC GAC GAT GAC CTC GAC CAG 1109
 Gly Arg Ile Arg Leu Pro Val Leu Gly Ser Asp Asp Asp Leu Asp Gln
 130 135 140
 35 CTC GAA ATC AGG GAC GGG GAG CTG CGG TAC TAC GAC CAC CGA TTC CCG 1157
 Leu Glu Ile Arg Asp Gly Glu Leu Arg Tyr Tyr Asp His Arg Phe Pro
 145 150 155 160
 40 CTC GCC GAG GGA ACC TAC GCC GAA GGC GAC GCC CCG CGG GAT GTC CAC 1205
 Leu Ala Glu Gly Thr Tyr Ala Glu Gly Asp Ala Pro Arg Asp Val His
 165 170 175
 45 GCC CGG CAG CAC TAC GAG CTC ATC GGC TGG CGC CGC GCG GAC AAC GAG 1253
 Ala Arg Gln His Tyr Glu Leu Ile Gly Trp Arg Arg Ala Asp Asn Glu
 180 185 190
 50 CTG AAC TAC CGC CGC TTT TTC GCG GTG AAC ACG CTC GCC GGC GTC CGC 1301
 Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu Ala Gly Val Arg
 55

5 195 200 205
 GTG GAA ATC CCC GCC GTC TTC GAC GAG GCA CAC CAG GAG GTG GTG CGC 1349
 Val Glu Ile Pro Ala Val Phe Asp Glu Ala His Gln Glu Val Val Arg
 10 210 215 220
 TGG TTC CGC GAG GAC CTT GCG GAC GGC CTG CGG ATC GAC CAC CCG GAC 1397
 Trp Phe Arg Glu Asp Leu Ala Asp Gly Leu Arg Ile Asp His Pro Asp
 15 225 230 235 240
 GGC CTC GCT GAC CCC GAG GGG TAC CTG AAG CGA CTC CGG GAA GTC ACC 1445
 Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val Thr
 20 245 250 255
 GGC GGC GCT TAC CTG CTG ATC GAA AAG ATC CTG GAG CCG GGG GAG CAG 1493
 Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln
 25 260 265 270
 CTG CCC GCC AGC TTC GAG TGT GAA GGC ACC ACA GGC TAC GAC GCC CTC 1541
 Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu
 30 275 280 285
 GCC GAC GTC GAC CGG GTT CTC GTG GAC CCG CGC GGC CAG GAA CCG CTG 1589
 Ala Asp Val Asp Arg Val Leu Val Asp Pro Arg Gly Gln Glu Pro Leu
 35 290 295 300
 GAC CGG CTT GAC GCG TCC CTG CGT GGC GGC GAG CCC GCC GAC TAC CAG 1637
 Asp Arg Leu Asp Ala Ser Leu Arg Gly Gly Glu Pro Ala Asp Tyr Gln
 40 305 310 315 320
 GAC ATG ATC CGC GGA ACC AAG CGC CGG ATC ACC GAC GGT ATC CTG CAC 1685
 Asp Met Ile Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His
 45 325 330 335
 TCG GAG ATC CTG CGG CTG GCC CGG CTG GTT CCG GGC GAC GCC AAC GTT 1733
 Ser Glu Ile Leu Arg Leu Ala Arg Leu Val Pro Gly Asp Ala Asn Val
 50 340 345 350
 TCA ATC GAC GCC GGA GCC GAC GCT CTC GCC GAA ATC ATC GCC GCC TTC 1781

5 Ser Ile Asp Ala Gly Ala Asp Ala Leu Ala Glu Ile Ile Ala Ala Phe
 355 360 365
 CCG GTC TAC CGC ACC TAC CTG CCG GAG GGC GCC GAG GTC CTG AAG GAG 1829
 10 Pro Val Tyr Arg Thr Tyr Leu Pro Glu Gly Ala Glu Val Leu Lys Glu
 370 375 380
 GCG TGC GAG CTT GCC GCG CGT AGG CGG CCG GAA CTC GAC CAG GCC ATC 1877
 15 Ala Cys Glu Leu Ala Ala Arg Arg Arg Pro Glu Leu Asp Gln Ala Ile
 385 390 395 400
 CAG GCT CTG CAG CCG CTG CTG CTG GAC ACG GAC CTC GAG CTT GCC CGG 1925
 20 Gln Ala Leu Gln Pro Leu Leu Leu Asp Thr Asp Leu Glu Leu Ala Arg
 405 410 415
 CGC TTC CAG CAG ACC TCG GGC ATG GTC ATG GCC AAG GGC GTG GAG GAC 1973
 25 Arg Phe Gln Gln Thr Ser Gly Met Val Met Ala Lys Gly Val Glu Asp
 420 425 430
 ACC GCG TTC TTC CGC TAC AAC CGC CTG GGC ACC CTC ACG GAA GTG GGC 2021
 30 Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly Thr Leu Thr Glu Val Gly
 435 440 445
 GCC GAC CCC ACC GAG TTC GCC GTG GAG CCG GAC GAG TTC CAC GCC CGG 2069
 35 Ala Asp Pro Thr Glu Phe Ala Val Glu Pro Asp Glu Phe His Ala Arg
 450 455 460
 CTG GCA CGC CGG CAG GCC GAG CTT CCG CTG TCC ATG ACG ACG CTG AGC 2117
 40 Leu Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met Thr Thr Leu Ser
 465 470 475 480
 ACG CAC GAC ACC AAG CGC AGC GAG GAC ACC CGA GCA AGG ATT TCG GTC 2165
 45 Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg Ile Ser Val
 485 490 495
 ATT TCC GAG GTT GCG GGT GAC TGG GAA AAG GCC TTG AAC CGG CTG CGC 2213
 50 Ile Ser Glu Val Ala Gly Asp Trp Glu Lys Ala Leu Asn Arg Leu Arg
 500 505 510

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5 GAC CTG GCC CCG CTG CCG GAC GGC CCG CTG TCC GCG CTG CTC TGG CAG 2261
 Asp Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Ala Leu Leu Trp Gln
 515 520 525
 10 GCC ATT GCC GGC GCC TGG CCC GCC AGC CGG GAA CGC CTG CAG TAC TAC 2309
 Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Tyr Tyr
 530 535 540
 15 GCG CTG AAG GCC GCG CGT GAA GCG GGG AAC TCG ACC AAC TGG ACC GAT 2357
 Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Asn Trp Thr Asp
 545 550 555 560
 20 CCG GCC CCC GCG TTC GAG GAG AAG CTG AAG GCC GCG GTC GAC GCC GTG 2405
 Pro Ala Pro Ala Phe Glu Glu Lys Leu Lys Ala Ala Val Asp Ala Val
 565 570 575
 25 TTC GAC AAT CCC GCC GTG CAG GCC GAG GTG GAA GCC CTC GTC GAG CTC 2453
 Phe Asp Asn Pro Ala Val Gln Ala Glu Val Glu Ala Leu Val Glu Leu
 580 585 590
 30 CTG GAG CCG TAC GGA GCT TCG AAC TCC CTC GCC GCC AAG CTC GTG CAG 2501
 Leu Glu Pro Tyr Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln
 595 600 605
 35 CTG ACC ATG CCC GGC GTC CCG GAC GTC TAC CAG GGC ACG GAG TTC TGG 2549
 Leu Thr Met Pro Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp
 610 615 620
 40 GAC CGG TCG CTG ACG GAC CCG GAC AAC CGG CGG CCG TTC AGC TTC GAC 2597
 Asp Arg Ser Leu Thr Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Asp
 625 630 635 640
 45 GAC CGC CGC GCC GCG CTG GAG CAG CTG GAT GCC GGC GAC CTT CCC GCG 2645
 Asp Arg Arg Ala Ala Leu Glu Gln Leu Asp Ala Gly Asp Leu Pro Ala
 645 650 655
 50 TCA TTT ACC GAT GAG CGG ACG AAG CTG CTA GTG ACG TCG CGC GCG CTG 2693
 Ser Phe Thr Asp Glu Arg Thr Lys Leu Leu Val Thr Ser Arg Ala Leu
 55

5 660 665 670
 CGG CTG CGC CGG GAC CGT CCG GAG CTG TTC ACG GGG TAC CGG CCG GTC 2741
 Arg Leu Arg Arg Asp Arg Pro Glu Leu Phe Thr Gly Tyr Arg Pro Val
 10 675 680 685
 CTG GCC AGC GGG CCC GCC GCC GGG CAC CTG CTC GCG TTC GAC CGC GGC 2789
 Leu Ala Ser Gly Pro Ala Ala Gly His Leu Leu Ala Phe Asp Arg Gly
 15 690 695 700
 ACC GCG GCG GCG CCG GGT GCA TTG ACC CTC GCC ACG CGG CTT CCC TAC 2837
 Thr Ala Ala Ala Pro Gly Ala Leu Thr Leu Ala Thr Arg Leu Pro Tyr
 20 705 710 715 720
 GGG CTG GAA CAG TCG GGT GGA TGG CGG GAC ACC GCC GTC GAA CTT AAC 2885
 Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr Ala Val Glu Leu Asn
 25 725 730 735
 ACC GCC ATG AAA GAC GAA CTG ACC GGT GCC GGC TTC GGA CCG GGG GCA 2933
 Thr Ala Met Lys Asp Glu Leu Thr Gly Ala Gly Phe Gly Pro Gly Ala
 30 740 745 750
 GTG AAG ATC GCC GAC ATC TTC CGG TCG TTC CCC GTT GCG CTG CTG GTG 2981
 Val Lys Ile Ala Asp Ile Phe Arg Ser Phe Pro Val Ala Leu Leu Val
 35 755 760 765
 CCG CAG ACA GGA GGA GAG TCA 3002
 Pro Gln Thr Gly Gly Glu Ser
 40 770 775
 TGACGCACAC CTACCCGCGG GAAGCCGCGA AACCCGTCCT GGGCCCCGCA CGCTACGACG 3062
 TCTGGGCGCC C 3073
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- 50 14. The replicable recombinant DNA as claimed in claim 8, wherein said DNA is derived from a microorganism selected from the group consisting of those of the genera *Rhizobium*, *Arthrobacter*, *Brevibacterium*, *Flavobacterium*, *Micrococcus*, *Curtobacterium*, *Mycobacterium* and *Terrabacter*.
 55 15. The recombinant DNA as claimed in claim 8, wherein said self-replicable vector is a plasmid vector Blue-script II SK(+).
 16. A transformant obtainable by introducing into a suitable host a recombinant DNA containing the DNA of claim 1 and a self-replicable vector.

17. The transformant as claimed in claim 16, wherein said DNA encodes an enzyme having the following physicochemical properties:

(1) Molecular weight

About 76,000-87,000 daltons on sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE); and

(2) Isoelectric point (pI)

About 3.6-4.6 on isoelectrophoresis.

18. The transformant as claimed in claim 16, wherein said DNA encodes an amino acid sequence selected from the group consisting of those as shown in the following SEQ ID NOs:2 and 4 that initiate from the N-terminal, and homologous amino acid sequences to these amino acid sequences:

SEQ ID NO:2

Met Arg Thr Pro Ala Ser Thr Tyr Arg Leu Gln Ile Arg Arg Gly Phe Thr

1 5 10 15

Leu Phe Asp Ala Ala Glu Thr Val Pro Tyr Leu Lys Ser Leu Gly Val Asp

20 25 30

Trp Ile Tyr Leu Ser Pro Ile Leu Lys Ala Glu Ser Gly Ser Asp His Gly

35 40 45 50

Tyr Asp Val Thr Asp Pro Ala Val Val Asp Pro Glu Arg Gly Gly Pro Glu

55 60 65

5 Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Gly Ala Gly Met Gly Val Leu
 70 75 80 85
 Ile Asp Ile Val Pro Asn His Val Gly Val Ala Ser Pro Pro Gln Asn Pro
 10 90 95 100
 Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg Gly Ser Pro Tyr Ala Val Ala
 105 110 115
 15 Phe Asp Val Asp Trp Asp Leu Ala Gly Gly Arg Ile Arg Ile Pro Val Leu
 120 125 130 135
 Gly Ser Asp Asp Asp Leu Asp Gln Leu Glu Ile Lys Asp Gly Glu Leu Arg
 20 140 145 150
 Tyr Tyr Asp His Arg Phe Pro Leu Ala Glu Gly Ser Tyr Arg Asp Gly Asp
 155 160 165 170
 25 Ser Pro Gln Asp Val His Gly Arg Gln His Tyr Glu Leu Ile Gly Trp Arg
 175 180 185
 Arg Ala Asp Asn Glu Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu
 30 190 195 200
 Ala Gly Ile Arg Val Glu Val Pro Pro Val Phe Asp Glu Ala His Gln Glu
 205 210 215 220
 35 Val Val Arg Trp Phe Arg Ala Gly Leu Ala Asp Gly Leu Arg Ile Asp His
 225 230 235
 Pro Asp Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val
 40 240 245 250 255
 Thr Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln
 260 265 270
 45 Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu Ala
 275 280 285
 Asp Val Asp Arg Val Phe Val Asp Pro Arg Gly Gln Val Pro Leu Asp Arg
 50 290 295 300 305
 Leu Asp Ala Arg Leu Arg Gly Gly Ala Pro Ala Asp Tyr Glu Asp Met Ile
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5 310 315 320
 Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His Ser Glu Ile Leu
 325 330 335 340
 10 Arg Leu Ala Arg Leu Val Pro Glu Gln Thr Gly Ile Pro Gly Glu Ala Ala
 345 350 355
 Ala Asp Ala Ile Ala Glu Ile Ile Ala Ala Phe Pro Val Tyr Arg Ser Tyr
 15 360 365 370
 Leu Pro Glu Gly Ala Glu Ile Leu Lys Glu Ala Cys Asp Leu Ala Ala Arg
 375 380 385 390
 20 Arg Arg Pro Glu Leu Gly Gln Thr Val Gln Leu Leu Gln Pro Leu Leu Leu
 395 400 405
 Asp Thr Asp Leu Glu Ile Ser Arg Arg Phe Gln Gln Thr Ser Gly Met Val
 25 410 415 420 425
 Met Ala Lys Gly Val Glu Asp Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly
 430 435 440
 30 Thr Leu Thr Glu Val Gly Ala Asp Pro Thr Glu Phe Ser Leu Glu Pro Glu
 445 450 455
 Glu Phe His Val Arg Met Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met
 35 460 465 470 475
 Thr Thr Leu Ser Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg
 480 485 490
 40 Ile Ser Val Ile Ala Glu Val Ala Pro Glu Trp Glu Lys Ala Leu Asp Arg
 495 500 505 510
 Leu Asn Thr Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Thr Leu Leu Trp
 45 515 520 525
 Gln Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Ser Tyr
 530 535 540
 50 Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Ser Trp Thr Asp Pro
 545 550 555 560
 55

5 Asp Pro Ala Phe Glu Glu Ala Leu Ser Ala Val Val Asp Ser Ala Phe Asp
 565 570 575
 Asn Pro Glu Val Arg Ala Glu Leu Glu Ala Leu Val Gly Leu Leu Ala Pro
 10 580 585 590 595
 His Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln Leu Thr Met Pro
 600 605 610
 15 Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp Asp Arg Ser Leu Thr
 615 620 625
 Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Ala Glu Arg Ile Arg Ala Leu
 20 630 635 640 645
 Asp Gln Leu Asp Ala Gly His Arg Pro Asp Ser Phe Gln Asp Glu Ala Val
 650 655 660
 25 Lys Leu Leu Val Thr Ser Arg Ala Leu Arg Leu Arg Arg Asn Arg Pro Glu
 665 670 675 680
 Leu Phe Thr Gly Tyr Arg Pro Val His Ala Arg Gly Pro Ala Ala Gly His
 30 685 690 695
 Leu Val Ala Phe Asp Arg Gly Ala Gly Gly Val Leu Ala Leu Ala Thr Arg
 700 705 710
 35 Leu Pro Tyr Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr Ala Val Glu
 715 720 725 730
 Leu Glu Ala Ala Met Thr Asp Glu Leu Thr Gly Ser Thr Phe Gly Pro Gly
 40 735 740 745
 Pro Ala Ala Leu Ser Glu Val Phe Arg Ala Tyr Pro Val Ala Leu Leu Val
 750 755 760 765
 45 Pro Ala Thr Gly Gly Lys Ser
 770

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SEQ ID NO:4

Met Arg Thr Pro Val Ser Thr Tyr Arg Leu Gln Ile Arg Lys Gly Phe Thr

5 1 5 10 15
 Leu Phe Asp Ala Ala Lys Thr Val Pro Tyr Leu His Ser Leu Gly Val Asp
 20 25 30
 10 Trp Val Tyr Leu Ser Pro Val Leu Thr Ala Glu Gln Gly Ser Asp His Gly
 35 40 45 50
 Tyr Asp Val Thr Asp Pro Ser Ala Val Asp Pro Glu Arg Gly Gly Pro Glu
 15 55 60 65
 Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Ala Ala Gly Met Gly Val Leu
 70 75 80 85
 20 Ile Asp Ile Val Pro Asn His Val Gly Val Ala Thr Pro Ala Gln Asn Pro
 90 95 100
 Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg Gln Ser Arg Tyr Ala Glu Ala
 25 105 110 115
 Phe Asp Val Asp Trp Asp Leu Ala Gly Gly Arg Ile Arg Leu Pro Val Leu
 120 125 130 135
 30 Gly Ser Asp Asp Asp Leu Asp Gln Leu Glu Ile Arg Asp Gly Glu Leu Arg
 140 145 150
 Tyr Tyr Asp His Arg Phe Pro Leu Ala Glu Gly Thr Tyr Ala Glu Gly Asp
 35 155 160 165 170
 Ala Pro Arg Asp Val His Ala Arg Gln His Tyr Glu Leu Ile Gly Trp Arg
 175 180 185
 40 Arg Ala Asp Asn Glu Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu
 190 195 200
 Ala Gly Val Arg Val Glu Ile Pro Ala Val Phe Asp Glu Ala His Gln Glu
 45 205 210 215 220
 Val Val Arg Trp Phe Arg Glu Asp Leu Ala Asp Gly Leu Arg Ile Asp His
 225 230 235
 50 Pro Asp Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val
 240 245 250 255
 55

5	Thr Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln			
	260	265	270	
10	Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu Ala			
	275	280	285	
15	Asp Val Asp Arg Val Leu Val Asp Pro Arg Gly Gln Glu Pro Leu Asp Arg			
	290	295	300	305
20	Leu Asp Ala Ser Leu Arg Gly Gly Glu Pro Ala Asp Tyr Gln Asp Met Ile			
	310	315	320	
25	Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His Ser Glu Ile Leu			
	325	330	335	340
30	Arg Leu Ala Arg Leu Val Pro Gly Asp Ala Asn Val Ser Ile Asp Ala Gly			
	345	350	355	
35	Ala Asp Ala Leu Ala Glu Ile Ile Ala Ala Phe Pro Val Tyr Arg Thr Tyr			
	360	365	370	
40	Leu Pro Glu Gly Ala Glu Val Leu Lys Glu Ala Cys Glu Leu Ala Ala Arg			
	375	380	385	390
45	Arg Arg Pro Glu Leu Asp Gln Ala Ile Gln Ala Leu Gln Pro Leu Leu Leu			
	395	400	405	
50	Asp Thr Asp Leu Glu Leu Ala Arg Arg Phe Gln Gln Thr Ser Gly Met Val			
	410	415	420	425
55	Met Ala Lys Gly Val Glu Asp Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly			
	430	435	440	
60	Thr Leu Thr Glu Val Gly Ala Asp Pro Thr Glu Phe Ala Val Glu Pro Asp			
	445	450	455	
65	Glu Phe His Ala Arg Leu Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met			
	460	465	470	475
70	Thr Thr Leu Ser Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg			
	480	485	490	
75	Ile Ser Val Ile Ser Glu Val Ala Gly Asp Trp Glu Lys Ala Leu Asn Arg			

5 495 500 505 510
 Leu Arg Asp Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Ala Leu Leu Trp
 515 520 525
 10 Gln Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Tyr Tyr
 530 535 540
 15 Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Asn Trp Thr Asp Pro
 545 550 555 560
 Ala Pro Ala Phe Glu Glu Lys Leu Lys Ala Ala Val Asp Ala Val Phe Asp
 565 570 575
 20 Asn Pro Ala Val Gln Ala Glu Val Glu Ala Leu Val Glu Leu Leu Glu Pro
 580 585 590 595
 25 Tyr Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln Leu Thr Met Pro
 600 605 610
 Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp Asp Arg Ser Leu Thr
 615 620 625
 30 Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Asp Asp Arg Arg Ala Ala Leu
 630 635 640 645
 35 Glu Gln Leu Asp Ala Gly Asp Leu Pro Ala Ser Phe Thr Asp Glu Arg Thr
 650 655 660
 Lys Leu Leu Val Thr Ser Arg Ala Leu Arg Leu Arg Arg Asp Arg Pro Glu
 665 670 675 680
 40 Leu Phe Thr Gly Tyr Arg Pro Val Leu Ala Ser Gly Pro Ala Ala Gly His
 685 690 695
 45 Leu Leu Ala Phe Asp Arg Gly Thr Ala Ala Ala Pro Gly Ala Leu Thr Leu
 700 705 710
 Ala Thr Arg Leu Pro Tyr Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr
 715 720 725 730
 50 Ala Val Glu Leu Asn Thr Ala Met Lys Asp Glu Leu Thr Gly Ala Gly Phe
 735 740 745

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Gly Pro Gly Ala Val Lys Ile Ala Asp Ile Phe Arg Ser Phe Pro Val Ala
 750 755 760 765

5 Leu Leu Val Pro Gln Thr Gly Gly Glu Ser
 770 775

- 10 19. The transformant as claimed in claim 16, wherein said DNA has a base sequence selected from the group consisting of those as shown in the following SEQ ID NOs:1 and 3 that initiate from the 5'-terminus, homologous base sequences to the base sequences, and complementary base sequences to these base sequences:

15 SEQ ID NO:1

20 ATGAGGACAC CCGCCTCGAC CTACCGGCTG CAGATCAGGC GGGGTTTCAC GCTGTTTGAT 60
 GCCGCCGAGA CCGTGCCCTA CCTGAAGTCA CTCGGGGTGG ACTGGATCTA CCTGTGCCCC 120
 ATCCTGAAGG CAGAGAGCGG CTCCGACCAC GGCTATGACG TCACCGATCC CGCCGTAGTG 180
 25 GACCCGGAGC GCGGCGGCCC TGAAGGGCTG GCCGCGGTGT CCAAGGCGGC CCGCGGTGCC 240
 GGCATGGGCG TGCTGATCGA CATCGTGCCG AACCACGTGG GCGTGCGGTC GCCGCCGACG 300
 AACCCGTGGT GGTGGTCGCT GCTCAAGGAA GGGCGCGGGT CGCCCTACGC CGTGGCGTTC 360
 30 GACGTCGACT GGGACCTGGC GGGGGGCCGC ATCCGGATCC CCGTCCTGGG CAGCGACGAC 420
 GATCTGGACC AGCTCGAAAT CAAGGACGGC GAGCTGCGGT ACTACGACCA CCGCTTCCCG 480
 CTGGCCGAGG GCAGCTACCG GGACGGCGAC TCCCCGCAGG ACGTCCACGG CCGGCAGCAC 540
 35 TACGAACTCA TCGGCTGGCG GCGCGCCGAC AATGAACTGA ACTACCGCCG GTTCTTCGCG 600
 GTGAACACGC TCGCCGGCAT CCGGGTGGAG GTGCCGCCGG TCTTCGATGA AGCGCACCAG 660
 GAGGTGGTGC GCTGGTTCCG TGCGGGGCTC GCCGACGGGC TGCGGATCGA CCACCCGGAC 720
 40 GGCCTGGCCG ATCCCGAGGG GTATTTGAAG CGGCTCCGTG AGGTCACCGG GGGCGCGTAC 780
 CTGCTCATCG AAAAGATCCT CGAGCCGGGC GAACAGTTGC CGGCCAGCTT CGAGTGCGAA 840
 GGCACCACCG GCTACGACGC CCTCGCGGAT GTCGACAGGG TCTTCGTGGA CCCGCGGGGA 900
 45 CAGGTGCCGC TGGACCGTCT GGACGCACGG CTGCGCGGCG GTGCGCCGGC CGACTACGAG 960
 GACATGATCC GCGGGACCAA GCGCCGGATC ACCGACGGCA TCCTGCACTC CGAGATCCTG 1020
 CGCCTTGCCA GGCTGGTGCC CGAGCAGACC GGAATTCCCG GGGAGGCGGC CGCGGATGCG 1080

5 ATCGCGGAGA TCATCGCGGC CTTCCCGGTC TACCGGTCCT ATCTTCCCGA GGGCGCGGAG 1140
 ATCCTGAAGG AGGCCTGCGA CCTCGCCGCG CGGAGGCGTC CGGAAGTGGG CCAGACCGTC 1200
 CAGCTGCTGC AGCCGCTGCT GCTGGATACC GACCTCGAGA TTTCCCGCAG GTTCCAGCAG 1260
 10 ACCTCGGGAA TGGTCATGGC CAAAGGCGTG GAGGACACCG CGTTCTTCCG CTACAACCGG 1320
 CTGGGAACGC TCACCGAGGT GGGCGCCGAC CCCACCGAGT TCTCGCTGGA ACCGGAGGAG 1380
 TTTACGTCC GGATGGCCCG CCGGCAGGCC GAACTCCCGC TCTCCATGAC CACCCTGAGC 1440
 15 ACGCACGACA CCAAGCGCAG CGAGGACACC CGGGCCCGGA TCTCGGTGAT CGCCGAGGTC 1500
 GCGCCTGAAT GGGAAAAGGC CCTGGACAGG CTGAACACCC TCGCTCCGCT GCCGGACGGC 1560
 CCGCTCTCCA CGCTGCTCTG GCAGGCGATT GCGGGGGCAT GGCCGGCCAG CCGGGAACGC 1620
 20 CTTCAATCCT ACGCCCTGAA AGCGGCGCGC GAAGCCGGGA ACTCGACCAG CTGGACCGAT 1680
 CCGGACCCCG CATTCGAGGA GGCACCTTCC GCCGTCGTCG ACTCCGCCTT CGACAATCCG 1740
 GAGGTGCGTG CGGAACCTGA GGCCCTGGTG GGCCTCCTTG CGCCGCACGG TCGTCCAAC 1800
 25 TCGCTCGCGG CAAAGCTTGT CCAGCTGACC ATGCCGGGCG TTCCGGACGT GTACCAGGGC 1860
 ACCGAGTTCT GGGACAGGTC GCTGACCGAT CCGGACAACC GGCGCCCTT CAGCTTCGCC 1920
 GAACGGATTA GGGCCTTGGA CCAGTTGGAC GCCGGCCACC GTCCGGACTC CTTCCAGGAC 1980
 30 GAGGCGGTCA AGCTGCTGGT CACCTCGAGG GCGCTGCGGC TCGGCGGAA CCGGCCCGAG 2040
 CTCTTCACCG GCTACCGCCC CGTGATGCC AGGGGCCCCG CCGCCGGGCA CCTGGTGGCG 2100
 TTCGACCGCG GCGCCGGGGG AGTGCTGGCG CTTGCCACCC GGCTCCCCTA CGGGCTGGAA 2160
 35 CAGTCGGGCG GCTGGCGGGA CACCGCCGTC GAGCTTGAAG CCGCCATGAC GGACGAACTG 2220
 ACCGGCTCCA CTTTCGGGCC GGGACCGGCG GCGCTGTCAG AAGTCTTCG GGCCTACCG 2280
 GTGGCCTTGT TGGTCCCCGC GACAGGAGGC AAGTCA 2316

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SEQ ID NO:3

5 ATGAGAACGC CAGTCTCCAC GTACAGGCTG CAGATCAGGA AGGGATTCAC ACTCTTCGAC 60
GCGGCCAAAA CCGTTCCGTA CCTGCACTCG CTCGGCGTCG ACTGGGTCTA CCTTTCTCCG 120
GTCCTGACTG CCGAGCAGGG CTCCGACCAC GGGTACGACG TCACCGATCC CTCCGCCGTC 180
10 GACCCCGAAC GCGGC GGGCC GGAGGGCCTC GCGGCGGTTT CCAAGGCGGC CCGCGCCGCG 240
GGCATGGGCG TGCTGATCGA CATCGTGCCC AACCACGTGG GCGTCGCGAC GCCGGCGCAG 300
AACCCTGGT GGTGGTCGCT GCTCAAGGAG GGACGCCAGT CCCGTTACGC GGAGGCGTTC 360
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5 GACGTCGATT GGGACCTCGC CGGGGGACGC ATCCGGCTGC CGGTGCTCGG CAGCGACGAT 420
 GACCTCGACC AGCTCGAAAT CAGGGACGGG GAGCTGCGGT ACTACGACCA CCGATTCCCG 480
 CTCGCCGAGG GAACCTACGC CGAAGGCGAC GCGCCGCGGG ATGTCCACGC CCGGCAGCAC 540
 10 TACGAGCTCA TCGGCTGGCG CCGCGCGGAC AACGAGCTGA ACTACCGCCG CTTTTTCGCG 600
 GTGAACACGC TCGCCGGCGT CCGCGTGGAA ATCCCCGCCG TCTTCGACGA GGCACACCAG 660
 GAGGTGGTGC GCTGGTTCCG CGAGGACCTT GCGGACGGCC TCGGATCGA CCACCCGGAC 720
 15 GGCCTCGCTG ACCCCGAGGG GTACCTGAAG CGACTCCGGG AAGTCACCGG CGGCGCTTAC 780
 CTGCTGATCG AAAAGATCCT GGAGCCGGGG GAGCAGCTGC CCGCCAGCTT CGAGTGTGAA 840
 GGCACCACAG GCTACGACGC CCTCGCCGAC GTCGACCGGG TTCTCGTGGG CCCGCGCGGC 900
 20 CAGGAACCGC TGGACCGGCT TGACGCGTCC CTGCGTGGCG GCGAGCCCGC CGACTACCAG 960
 GACATGATCC GCGGAACCAA GCGCCGGATC ACCGACGGTA TCCTGCACTC GGAGATCCTG 1020
 CGGCTGGCCC GGCTGGTTCC GGGCGACGCC AACGTTTCAA TCGACGCCGG AGCCGACGCT 1080
 25 CTCGCCGAAA TCATCGCCGC CTTCCCGGTC TACCGCACCT ACCTGCCGGA GGGCGCCGAG 1140
 GTCCTGAAGG AGGCGTGCGA GCTTGCCGCG CGTAGCGGCG CGGAACTCGA CCAGGCCATC 1200
 CAGGCTCTGC AGCCGCTGCT GCTGGACACG GACCTCGAGC TTGCCCGGCG CTTCCAGCAG 1260
 30 ACCTCGGGCA TGGTCATGGC CAAGGGCGTG GAGGACACCG CGTTCTTCCG CTACAACCGC 1320
 CTGGGCACCC TCACGGAAGT GGGCGCCGAC CCCACCGAGT TCGCCGTGGA GCCGGACGAG 1380
 TTCCACGCCC GGCTGGCACG CCGGCAGGCC GAGCTTCCGC TGTCCATGAC GACGCTGAGC 1440
 35 ACGCACGACA CCAAGCGCAG CGAGGACACC CGAGCAAGGA TTTCCGGTCAT TTCCGAGGTT 1500
 GCGGGTGACT GGGAAAAGGC CTTGAACCGG CTGCGCGACC TGGCCCCGCT GCCGGACGGC 1560
 CCGCTGTCCG CGCTGCTCTG GCAGGCCATT GCCGGCGCCT GGCCCCGCGC CCGGGAACGC 1620
 40 CTGCAGTACT ACGCGCTGAA GGCCGCGCGT GAAGCGGGGA ACTCGACCAA CTGGACCGAT 1680
 CCGGCCCCCG CGTTCGAGGA GAAGCTGAAG GCCGCGGTCTG ACGCCGTGTT CGACAATCCC 1740
 GCCGTGCAGG CCGAGGTGGA AGCCCTCGTC GAGCTCCTGG AGCCGTACGG AGCTTCGAAC 1800
 45 TCCCTCGCCG CCAAGCTCGT GCAGCTGACC ATGCCCGGCG TCCCGGACGT CTACCAGGGC 1860
 ACGGAGTTCT GGGACCGGTC GCTGACGGAC CCGGACAACC GCGGCGCGTT CAGCTTCGAC 1920
 50 GACCGCCCGC CCGCGCTGGA GCAGCTGGAT GCCGGCGACC TTCCCGCGTC ATTTACCGAT 1980
 GAGCGGACGA AGCTGCTAGT GACGTGCGCG GCGCTGCGGC TCGCGCGGGA CCGTCCGGAG 2040
 CTGTTACAGG GGTACCGGCC GGTCTGGCC AGCGGGCCCG CCGCCGGGCA CCTGCTCGCG 2100

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TTCGACCGCG GCACCGCGGC GCGCCGGGT GCATTGACCC TCGCCACGCG GCTTCCCTAC 2160
 GGGCTGGAAC AGTCGGGTGG ATGGCGGGAC ACCGCCGTGC AACTTAACAC CGCCATGAAA 2220
 5 GACGAACTGA CCGGTGCCGG CTTCGGACCG GGGGCAGTGA AGATCGCCGA CATCTCCGG-2280
 TCGTTCCCCG TTGCGCTGCT GGTGCCGCAG ACAGGAGGAG AGTCA 2325

- 10 20. The transformant as claimed in claim 19, wherein one or more bases in SEQ ID NOs:1 and 3 are replaced with other bases by means of degeneracy of genetic code without alternating their corresponding amino acid sequences as shown in the following SEQ ID NOs:2 and 4:

15 SEQ ID NO:2

20 Met Arg Thr Pro Ala Ser Thr Tyr Arg Leu Gln Ile Arg Arg Gly Phe Thr
 1 5 10 15
 Leu Phe Asp Ala Ala Glu Thr Val Pro Tyr Leu Lys Ser Leu Gly Val Asp
 20 25 30
 25 Trp Ile Tyr Leu Ser Pro Ile Leu Lys Ala Glu Ser Gly Ser Asp His Gly
 35 40 45 50
 Tyr Asp Val Thr Asp Pro Ala Val Val Asp Pro Glu Arg Gly Gly Pro Glu
 30 55 60 65
 Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Gly Ala Gly Met Gly Val Leu
 70 75 80 85
 35 Ile Asp Ile Val Pro Asn His Val Gly Val Ala Ser Pro Pro Gln Asn Pro
 90 95 100
 Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg Gly Ser Pro Tyr Ala Val Ala
 40 105 110 115
 Phe Asp Val Asp Trp Asp Leu Ala Gly Gly Arg Ile Arg Ile Pro Val Leu
 120 125 130 135
 45 Gly Ser Asp Asp Asp Leu Asp Gln Leu Glu Ile Lys Asp Gly Glu Leu Arg
 140 145 150
 Tyr Tyr Asp His Arg Phe Pro Leu Ala Glu Gly Ser Tyr Arg Asp Gly Asp
 50 155 160 165 170

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5 Ser Pro Gln Asp Val His Gly Arg Gln His Tyr Glu Leu Ile Gly Trp Arg
 175 180 185
 Arg Ala Asp Asn Glu Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu
 10 190 195 200
 Ala Gly Ile Arg Val Glu Val Pro Pro Val Phe Asp Glu Ala His Gln Glu
 205 210 215 220
 15 Val Val Arg Trp Phe Arg Ala Gly Leu Ala Asp Gly Leu Arg Ile Asp His
 225 230 235
 Pro Asp Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val
 20 240 245 250 255
 Thr Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln
 260 265 270
 25 Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu Ala
 275 280 285
 Asp Val Asp Arg Val Phe Val Asp Pro Arg Gly Gln Val Pro Leu Asp Arg
 30 290 295 300 305
 Leu Asp Ala Arg Leu Arg Gly Gly Ala Pro Ala Asp Tyr Glu Asp Met Ile
 310 315 320
 35 Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His Ser Glu Ile Leu
 325 330 335 340
 40 Arg Leu Ala Arg Leu Val Pro Glu Gln Thr Gly Ile Pro Gly Glu Ala Ala
 345 350 355
 Ala Asp Ala Ile Ala Glu Ile Ile Ala Ala Phe Pro Val Tyr Arg Ser Tyr
 360 365 370
 45 Leu Pro Glu Gly Ala Glu Ile Leu Lys Glu Ala Cys Asp Leu Ala Ala Arg
 375 380 385 390
 50 Arg Arg Pro Glu Leu Gly Gln Thr Val Gln Leu Leu Gln Pro Leu Leu Leu
 395 400 405
 Asp Thr Asp Leu Glu Ile Ser Arg Arg Phe Gln Gln Thr Ser Gly Met Val
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5 410 415 420 425
 Met Ala Lys Gly Val Glu Asp Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly
 430 435 440
 10 Thr Leu Thr Glu Val Gly Ala Asp Pro Thr Glu Phe Ser Leu Glu Pro Glu
 445 450 455
 15 Glu Phe His Val Arg Met Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met
 460 465 470 475
 Thr Thr Leu Ser Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg
 480 485 490
 20 Ile Ser Val Ile Ala Glu Val Ala Pro Glu Trp Glu Lys Ala Leu Asp Arg
 495 500 505 510
 25 Leu Asn Thr Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Thr Leu Leu Trp
 515 520 525
 Gln Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Ser Tyr
 530 535 540
 30 Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Ser Trp Thr Asp Pro
 545 550 555 560
 35 Asp Pro Ala Phe Glu Glu Ala Leu Ser Ala Val Val Asp Ser Ala Phe Asp
 565 570 575
 Asn Pro Glu Val Arg Ala Glu Leu Glu Ala Leu Val Gly Leu Leu Ala Pro
 580 585 590 595
 40 His Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln Leu Thr Met Pro
 600 605 610
 45 Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp Asp Arg Ser Leu Thr
 615 620 625
 Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Ala Glu Arg Ile Arg Ala Leu
 630 635 640 645
 50 Asp Gln Leu Asp Ala Gly His Arg Pro Asp Ser Phe Gln Asp Glu Ala Val
 650 655 660
 55

Lys Leu Leu Val Thr Ser Arg Ala Leu Arg Leu Arg Arg Asn Arg Pro Glu
 5 665 670 675 680
 Leu Phe Thr Gly Tyr Arg Pro Val His Ala Arg Gly Pro Ala Ala Gly His
 685 690 695
 10 Leu Val Ala Phe Asp Arg Gly Ala Gly Gly Val Leu Ala Leu Ala Thr Arg
 700 705 710
 Leu Pro Tyr Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr Ala Val Glu
 15 715 720 725 730
 Leu Glu Ala Ala Met Thr Asp Glu Leu Thr Gly Ser Thr Phe Gly Pro Gly
 735 740 745
 20 Pro Ala Ala Leu Ser Glu Val Phe Arg Ala Tyr Pro Val Ala Leu Leu Val
 750 755 760 765
 Pro Ala Thr Gly Gly Lys Ser
 25 770

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SEQ ID NO:4

5 Met Arg Thr Pro Val Ser Thr Tyr Arg Leu Gln Ile Arg Lys Gly Phe Thr
 1 5 10 15
 10 Leu Phe Asp Ala Ala Lys Thr Val Pro Tyr Leu His Ser Leu Gly Val Asp
 20 25 30
 Trp Val Tyr Leu Ser Pro Val Leu Thr Ala Glu Gln Gly Ser Asp His Gly
 35 40 45 50
 15 Tyr Asp Val Thr Asp Pro Ser Ala Val Asp Pro Glu Arg Gly Gly Pro Glu
 55 60 65
 20 Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Ala Ala Gly Met Gly Val Leu
 70 75 80 85
 Ile Asp Ile Val Pro Asn His Val Gly Val Ala Thr Pro Ala Gln Asn Pro
 90 95 100
 25 Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg Gln Ser Arg Tyr Ala Glu Ala
 30
 35
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 45
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5 105 110 115
 Phe Asp Val Asp Trp Asp Leu Ala Gly Gly Arg Ile Arg Leu Pro Val Leu
 120 125 130 135
 10 Gly Ser Asp Asp Asp Leu Asp Gln Leu Glu Ile Arg Asp Gly Glu Leu Arg
 140 145 150
 Tyr Tyr Asp His Arg Phe Pro Leu Ala Glu Gly Thr Tyr Ala Glu Gly Asp
 15 155 160 165 170
 Ala Pro Arg Asp Val His Ala Arg Gln His Tyr Glu Leu Ile Gly Trp Arg
 175 180 185
 20 Arg Ala Asp Asn Glu Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu
 190 195 200
 Ala Gly Val Arg Val Glu Ile Pro Ala Val Phe Asp Glu Ala His Gln Glu
 25 205 210 215 220
 Val Val Arg Trp Phe Arg Glu Asp Leu Ala Asp Gly Leu Arg Ile Asp His
 225 230 235
 30 Pro Asp Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val
 240 245 250 255
 35 Thr Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln
 260 265 270
 Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu Ala
 275 280 285
 40 Asp Val Asp Arg Val Leu Val Asp Pro Arg Gly Gln Glu Pro Leu Asp Arg
 290 295 300 305
 45 Leu Asp Ala Ser Leu Arg Gly Gly Glu Pro Ala Asp Tyr Gln Asp Met Ile
 310 315 320
 Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His Ser Glu Ile Leu
 50 325 330 335 340
 Arg Leu Ala Arg Leu Val Pro Gly Asp Ala Asn Val Ser Ile Asp Ala Gly
 345 350 355

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5 Ala Asp Ala Leu Ala Glu Ile Ile Ala Ala Phe Pro Val Tyr Arg Thr Tyr
 360 365 370
 Leu Pro Glu Gly Ala Glu Val Leu Lys Glu Ala Cys Glu Leu Ala Ala Arg
 10 375 380 385 390
 Arg Arg Pro Glu Leu Asp Gln Ala Ile Gln Ala Leu Gln Pro Leu Leu Leu
 395 400 405
 15 Asp Thr Asp Leu Glu Leu Ala Arg Arg Phe Gln Gln Thr Ser Gly Met Val
 410 415 420 425
 Met Ala Lys Gly Val Glu Asp Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly
 20 430 435 440
 Thr Leu Thr Glu Val Gly Ala Asp Pro Thr Glu Phe Ala Val Glu Pro Asp
 445 450 455
 25 Glu Phe His Ala Arg Leu Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met
 460 465 470 475
 Thr Thr Leu Ser Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg
 30 480 485 490
 Ile Ser Val Ile Ser Glu Val Ala Gly Asp Trp Glu Lys Ala Leu Asn Arg
 495 500 505 510
 35 Leu Arg Asp Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Ala Leu Leu Trp
 515 520 525
 40 Gln Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Tyr Tyr
 530 535 540
 Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Asn Trp Thr Asp Pro
 45 545 550 555 560
 Ala Pro Ala Phe Glu Glu Lys Leu Lys Ala Ala Val Asp Ala Val Phe Asp
 565 570 575
 50 Asn Pro Ala Val Gln Ala Glu Val Glu Ala Leu Val Glu Leu Leu Glu Pro
 580 585 590 595
 Tyr Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln Leu Thr Met Pro

5 600 605 610
 Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp Asp Arg Ser Leu Thr
 615 620 625
 10 Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Asp Asp Arg Arg Ala Ala Leu
 630 635 640 645
 Glu Gln Leu Asp Ala Gly Asp Leu Pro Ala Ser Phe Thr Asp Glu Arg Thr
 650 655 660
 15 Lys Leu Leu Val Thr Ser Arg Ala Leu Arg Leu Arg Arg Asp Arg Pro Glu
 665 670 675 680
 20 Leu Phe Thr Gly Tyr Arg Pro Val Leu Ala Ser Gly Pro Ala Ala Gly His
 685 690 695
 Leu Leu Ala Phe Asp Arg Gly Thr Ala Ala Ala Pro Gly Ala Leu Thr Leu
 700 705 710
 25 Ala Thr Arg Leu Pro Tyr Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr
 715 720 725 730
 30 Ala Val Glu Leu Asn Thr Ala Met Lys Asp Glu Leu Thr Gly Ala Gly Phe
 735 740 745
 Gly Pro Gly Ala Val Lys Ile Ala Asp Ile Phe Arg Ser Phe Pro Val Ala
 35 750 755 760 765
 Leu Leu Val Pro Gln Thr Gly Gly Glu Ser
 770 775
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21. The transformant as claimed in claim 16, wherein said DNA has a base sequence selected from the group consisting of those as shown in the following SEQ ID NOs:10 and 11:

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SEQ ID NO:10:

50 CGTGCTCTAC TTCAACGCGC ACGACGGCGA CGTCGTGTTC AAGCTCCCGT CGGATGAATA 60
 CGCCCCGGCC TGGGACGTCA TCATCGACAC CGCCGGCGCG GGTGCCGATT CCGAACCCGT 120
 GCAGGCTGGC GGCAAACCTCA CCGTGGCAGC GAAATCGCTC GTGGTGCTCC GTGCCACAG 180
 55 CGCCCCGGAG GAGGAACCGG ACCACTCGGT GGCCGCCTCC CTCGCAGCGC TGACGCAGAC 240

5 TGCGACCGCC GAAACCGCGG CGCTCACCGC CCCCACCGTT CCGGAGCCGA GGAAGACCAA 300
 GAAGGCAGCG CCGAAGCCGG AAGAGGAGGC TCCCAGACGAG GCGGCGCCGA AGCCGGAAGA 360
 10 GAAGGCTCCC GACGAGGCGG CGGCGAAGCC GGAAGAGGCT GCTTCCGACG AGGCGGCGGC 420
 GAAGCCGGAA GAGAAGGCTC CCGACGAGGC GCGGCGGAAG CCGGAAGAGG CTGCTTCCGA 480
 CGAGGCGGCG GCGAAGCCCG CGGGGAAGGC AGCGGCCAAA ACGGCCGGCA GGCGAGCGCC 540
 15 AGGCAAGCAG GGCGGGACGG GCTC 564
 ATG AGG ACA CCC GCC TCG ACC TAC CGG CTG CAG ATC AGG CGG GGT TTC 612
 Met Arg Thr Pro Ala Ser Thr Tyr Arg Leu Gln Ile Arg Arg Gly Phe
 20 1 5 10 15
 ACG CTG TTT GAT GCC GCC GAG ACC GTG CCC TAC CTG AAG TCA CTC GGG 660
 Thr Leu Phe Asp Ala Ala Glu Thr Val Pro Tyr Leu Lys Ser Leu Gly
 25 20 25 30
 GTG GAC TGG ATC TAC CTG TCG CCC ATC CTG AAG GCA GAG AGC GGC TCC 708
 Val Asp Trp Ile Tyr Leu Ser Pro Ile Leu Lys Ala Glu Ser Gly Ser
 30 35 40 45
 GAC CAC GGC TAT GAC GTC ACC GAT CCC GCC GTA GTG GAC CCG GAG CGC 756
 Asp His Gly Tyr Asp Val Thr Asp Pro Ala Val Val Asp Pro Glu Arg
 35 50 55 60
 GGC GGC CCT GAA GGG CTG GCC GCG GTG TCC AAG GCG GCC CGC GGT GCC 804
 Gly Gly Pro Glu Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Gly Ala
 40 65 70 75 80
 GGC ATG GGC GTG CTG ATC GAC ATC GTG CCG AAC CAC GTG GGC GTG GCG 852
 Gly Met Gly Val Leu Ile Asp Ile Val Pro Asn His Val Gly Val Ala
 45 85 90 95
 TCG CCG CCG CAG AAC CCG TGG TGG TGG TCG CTG CTC AAG GAA GGG CGC 900
 Ser Pro Pro Gln Asn Pro Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg
 50 100 105 110
 GGG TCG CCC TAC GCC GTG GCG TTC GAC GTC GAC TGG GAC CTG GCG GGG 948
 Gly Ser Pro Tyr Ala Val Ala Phe Asp Val Asp Trp Asp Leu Ala Gly
 55

5 115 120 125
 GGC CGC ATC CGG ATC CCC GTC CTG GGC AGC GAC GAC GAT CTG GAC CAG 996
 Gly Arg Ile Arg Ile Pro Val Leu Gly Ser Asp Asp Asp Leu Asp Gln
 10 130 135 140
 CTC GAA ATC AAG GAC GGC GAG CTG CGG TAC TAC GAC CAC CGC TTC CCG 1044
 Leu Glu Ile Lys Asp Gly Glu Leu Arg Tyr Tyr Asp His Arg Phe Pro
 15 145 150 155 160
 CTG GCC GAG GGC AGC TAC CGG GAC GGC GAC TCC CCG CAG GAC GTC CAC 1092
 Leu Ala Glu Gly Ser Tyr Arg Asp Gly Asp Ser Pro Gln Asp Val His
 20 165 170 175
 GGC CGG CAG CAC TAC GAA CTC ATC GGC TGG CGG CGC GCC GAC AAT GAA 1140
 Gly Arg Gln His Tyr Glu Leu Ile Gly Trp Arg Arg Ala Asp Asn Glu
 25 180 185 190
 CTG AAC TAC CGC CGG TTC TTC GCG GTG AAC ACG CTC GCC GGC ATC CGG 1188
 Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu Ala Gly Ile Arg
 30 195 200 205
 GTG GAG GTG CCG CCG GTC TTC GAT GAA GCG CAC CAG GAG GTG GTG CGC 1236
 Val Glu Val Pro Pro Val Phe Asp Glu Ala His Gln Glu Val Val Arg
 35 210 215 220
 TGG TTC CGT GCG GGG CTC GCC GAC GGG CTG CGG ATC GAC CAC CCG GAC 1284
 Trp Phe Arg Ala Gly Leu Ala Asp Gly Leu Arg Ile Asp His Pro Asp
 40 225 230 235 240
 GGC CTG GCC GAT CCC GAG GGG TAT TTG AAG CGG CTC CGT GAG GTC ACC 1332
 Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val Thr
 45 245 250 255
 GGG GGC GCG TAC CTG CTC ATC GAA AAG ATC CTC GAG CCG GGC GAA CAG 1380
 Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln
 50 260 265 270
 TTG CCG GCC AGC TTC GAG TGC GAA GGC ACC ACC GGC TAC GAC GCC CTC 1428

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Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu

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GCG GAT GTC GAC AGG GTC TTC GTG GAC CCG CGG GGA CAG GTG CCG CTG 1476

Ala Asp Val Asp Arg Val Phe Val Asp Pro Arg Gly Gln Val Pro Leu

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GAC CGT CTG GAC GCA CGG CTG CGC GGC GGT GCG CCG GCC GAC TAC GAG 1524

Asp Arg Leu Asp Ala Arg Leu Arg Gly Gly Ala Pro Ala Asp Tyr Glu

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GAC ATG ATC CGC GGG ACC AAG CGC CGG ATC ACC GAC GGC ATC CTG CAC 1572

Asp Met Ile Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His

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TCC GAG ATC CTG CGC CTT GCC AGG CTG GTG CCC GAG CAG ACC GGA ATT 1620

Ser Glu Ile Leu Arg Leu Ala Arg Leu Val Pro Glu Gln Thr Gly Ile

340

345

350

30

CCC GGG GAG GCG GCC GCG GAT GCG ATC GCG GAG ATC ATC GCG GCC TTC 1668

Pro Gly Glu Ala Ala Ala Asp Ala Ile Ala Glu Ile Ile Ala Ala Phe

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365

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CCG GTC TAC CGG TCC TAT CTT CCC GAG GGC GCG GAG ATC CTG AAG GAG 1716

Pro Val Tyr Arg Ser Tyr Leu Pro Glu Gly Ala Glu Ile Leu Lys Glu

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GCC TGC GAC CTC GCC GCG CGG AGG CGT CCG GAA CTG GGC CAG ACC GTC 1764

Ala Cys Asp Leu Ala Ala Arg Arg Arg Pro Glu Leu Gly Gln Thr Val

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CAG CTG CTG CAG CCG CTG CTG CTG GAT ACC GAC CTC GAG ATT TCC CGC 1812

Gln Leu Leu Gln Pro Leu Leu Leu Asp Thr Asp Leu Glu Ile Ser Arg

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AGG TTC CAG CAG ACC TCG GGA ATG GTC ATG GCC AAA GGC GTG GAG GAC 1860

Arg Phe Gln Gln Thr Ser Gly Met Val Met Ala Lys Gly Val Glu Asp

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5 ACC GCG TTC TTC CGC TAC AAC CGG CTG GGA ACG CTC ACC GAG GTG GGC 1908
 Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly Thr Leu Thr Glu Val Gly
 435 440 445
 10 GCC GAC CCC ACC GAG TTC TCG CTG GAA CCG GAG GAG TTT CAC GTC CGG 1956
 Ala Asp Pro Thr Glu Phe Ser Leu Glu Pro Glu Glu Phe His Val Arg
 450 455 460
 15 ATG GCC CGC CGG CAG GCC GAA CTC CCG CTC TCC ATG ACC ACC CTG AGC 2004
 Met Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met Thr Thr Leu Ser
 465 470 475 480
 20 ACG CAC GAC ACC AAG CGC AGC GAG GAC ACC CGG GCC CGG ATC TCG GTG 2052
 Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg Ile Ser Val
 485 490 495
 25 ATC GCC GAG GTC GCG CCT GAA TGG GAA AAG GCC CTG GAC AGG CTG AAC 2100
 Ile Ala Glu Val Ala Pro Glu Trp Glu Lys Ala Leu Asp Arg Leu Asn
 500 505 510
 30 ACC CTC GCT CCG CTG CCG GAC GGC CCG CTC TCC ACG CTG CTC TGG CAG 2148
 Thr Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Thr Leu Leu Trp Gln
 515 520 525
 35 GCG ATT GCG GGG GCA TGG CCG GCC AGC CGG GAA CGC CTT CAG TCC TAC 2196
 Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Ser Tyr
 530 535 540
 40 GCC CTG AAA GCG GCG CGC GAA GCC GGG AAC TCG ACC AGC TGG ACC GAT 2244
 Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Ser Trp Thr Asp
 545 550 555 560
 45 CCG GAC CCG GCA TTC GAG GAG GCA CTT TCC GCC GTC GTC GAC TCC GCC 2292
 Pro Asp Pro Ala Phe Glu Glu Ala Leu Ser Ala Val Val Asp Ser Ala
 565 570 575
 50 TTC GAC AAT CCG GAG GTG CGT GCG GAA CTT GAG GCC CTG GTG GGC CTC 2340
 Phe Asp Asn Pro Glu Val Arg Ala Glu Leu Glu Ala Leu Val Gly Leu
 55

5 580 585 590
 CTT GCG CCG CAC GGT GCG TCC AAC TCG CTC GCG GCA AAG CTT GTC CAG 2388
 Leu Ala Pro His Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln
 10 595 600 605
 CTG ACC ATG CCG GGC GTT CCG GAC GTG TAC CAG GGC ACC GAG TTC TGG 2436
 Leu Thr Met Pro Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp
 15 610 615 620
 GAC AGG TCG CTG ACC GAT CCG GAC AAC CGG CGC CCC TTC AGC TTC GCC 2484
 Asp Arg Ser Leu Thr Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Ala
 20 625 630 635 640
 GAA CGG ATT AGG GCC TTG GAC CAG TTG GAC GCC GGC CAC CGT CCG GAC 2532
 Glu Arg Ile Arg Ala Leu Asp Gln Leu Asp Ala Gly His Arg Pro Asp
 25 645 650 655
 TCC TTC CAG GAC GAG GCG GTC AAG CTG CTG GTC ACC TCG AGG GCG CTG 2580
 Ser Phe Gln Asp Glu Ala Val Lys Leu Leu Val Thr Ser Arg Ala Leu
 30 660 665 670
 CGG CTG CGG CGG AAC CGG CCC GAG CTC TTC ACC GGC TAC CGC CCC GTG 2628
 Arg Leu Arg Arg Asn Arg Pro Glu Leu Phe Thr Gly Tyr Arg Pro Val
 35 675 680 685
 CAT GCC AGG GGC CCC GCC GCC GGG CAC CTG GTG GCG TTC GAC CGC GGC 2676
 His Ala Arg Gly Pro Ala Ala Gly His Leu Val Ala Phe Asp Arg Gly
 40 690 695 700
 GCC GGG GGA GTG CTG GCG CTT GCC ACC CGG CTC CCC TAC GGG CTG GAA 2724
 Ala Gly Gly Val Leu Ala Leu Ala Thr Arg Leu Pro Tyr Gly Leu Glu
 45 705 710 715 720
 CAG TCG GGC GGC TGG CGG GAC ACC GCC GTC GAG CTT GAA GCC GCC ATG 2772
 Gln Ser Gly Gly Trp Arg Asp Thr Ala Val Glu Leu Glu Ala Ala Met
 50 725 730 735
 ACG GAC GAA CTG ACC GGC TCC ACT TTC GGG CCG GGA CCG GCG GCG CTG 2820
 55

Thr Asp Glu Leu Thr Gly Ser Thr Phe Gly Pro Gly Pro Ala Ala Leu
 740 745 750
 5 TCA GAA GTC TTC CGG GCC TAC CCG GTG GCC TTG TTG GTC CCC GCG ACA 2868
 Ser Glu Val Phe Arg Ala Tyr Pro Val Ala Leu Leu Val Pro Ala Thr
 755 760 765
 10 GGA GGC AAG TCA 2880
 Gly Gly Lys Ser
 770
 15 TGACGCAGCC CAACGATGCG GCCAAGCCGG TGCAGGGAGC GGGGCGCTTC GATATC 2936
 20
 25 SEQ ID NO:11
 GATCCGGACG GCAACCTCAT GTCCCCGGAG GACTGGGACA GCGGCTTCGG CCGTTCGGTG 60
 GGCATGTTCC TCAACGGCGA CGGCATCCAG GGCCACGATG ACCGCGGCCG CCGCATCACG 120
 30 GACGTGAACT TCCTGCTGTA CTTCAACGCC CACGACGGCG ACGTCGAGTT CACGCTGCCG 180
 CCGGACGAAT ACGCCCCGGC CTGGGACGTC ATCATCGACA CCGCCGGTGA AGGGGCCGAC 240
 TCCAAGCCCCG CGGACGCCGG AACCATCCTG TCCGTTGCGG CCAAGTCGCT GGTGTGCTT 300
 35 CGCGCCCACA GCGCACEGGA GGAGGAGCCT GACCATTCCG TGGCTGCTTC CCTGGCTGCA 360
 CTGACGCAGA CCGCCACCGC CGAGACGGCG GCGCTCACAG CTCCTGCCGT TCCGAGCCG 420
 GCCAAGACGA AGAAGCCGGC CGCTGACCCG GTTGCTGAAC CGGCCGACCC GCCGGTTGCT 480
 40 GACCCGGCCG ACCCGGTTGC TGACCCGGTT GCTGACCCGG CGCCGGAACC GGCTGCGGAG 540
 CCTGCGAAAT CCGCAGCGGA ACCTGGTGCG GAGCCTGCGA AGGACCCGGA GGAGCAGCCG 600
 GCGGAAAAGC CGGCGCGCAA GCCTGCGGCA AAGCGGGCG GCCACCTGAG GCGGTCAAG 660
 45 CCCGCTGGGG AGGACGC 677
 ATG AGA ACG CCA GTC TCC ACG TAC AGG CTG CAG ATC AGG AAG GGA TTC 725
 Met Arg Thr Pro Val Ser Thr Tyr Arg Leu Gln Ile Arg Lys Gly Phe
 50 1 5 10 15
 ACA CTC TTC GAC GCG GCC AAA ACC GTT CCG TAC CTG CAC TCG CTC GGC 773
 Thr Leu Phe Asp Ala Ala Lys Thr Val Pro Tyr Leu His Ser Leu Gly
 55 20 25 30

5 GTC GAC TGG GTC TAC CTT TCT CCG GTC CTG ACT GCC GAG CAG GGC TCC 821
 Val Asp Trp Val Tyr Leu Ser Pro Val Leu Thr Ala Glu Gln Gly Ser
 35 40 45
 10 GAC CAC GGG TAC GAC GTC ACC GAT CCC TCC GCC GTC GAC CCC GAA CGC 869
 Asp His Gly Tyr Asp Val Thr Asp Pro Ser Ala Val Asp Pro Glu Arg
 50 55 60
 15 GGC GGG CCG GAG GGC CTC GCG GCG GTT TCC AAG GCG GCC CGC GCC GCG 917
 Gly Gly Pro Glu Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Ala Ala
 65 70 75 80
 20 GGC ATG GGC GTG CTG ATC GAC ATC GTG CCC AAC CAC GTG GGC GTC GCG 965
 Gly Met Gly Val Leu Ile Asp Ile Val Pro Asn His Val Gly Val Ala
 85 90 95
 25 ACG CCG GCG CAG AAC CCC TGG TGG TGG TCG CTG CTC AAG GAG GGA CGC 1013
 Thr Pro Ala Gln Asn Pro Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg
 100 105 110
 30 CAG TCC CGT TAC GCG GAG GCG TTC GAC GTC GAT TGG GAC CTC GCC GGC 1061
 Gln Ser Arg Tyr Ala Glu Ala Phe Asp Val Asp Trp Asp Leu Ala Gly
 115 120 125
 35 GGA CGC ATC CGG CTG CCG GTG CTC GGC AGC GAC GAT GAC CTC GAC CAG 1109
 Gly Arg Ile Arg Leu Pro Val Leu Gly Ser Asp Asp Asp Leu Asp Gln
 130 135 140
 40 CTC GAA ATC AGG GAC GGG GAG CTG CGG TAC TAC GAC CAC CGA TTC CCG 1157
 Leu Glu Ile Arg Asp Gly Glu Leu Arg Tyr Tyr Asp His Arg Phe Pro
 145 150 155 160
 45 CTC GCC GAG GGA ACC TAC GCC GAA GGC GAC GCC CCG CGG GAT GTC CAC 1205
 Leu Ala Glu Gly Thr Tyr Ala Glu Gly Asp Ala Pro Arg Asp Val His
 165 170 175
 50 GCC CGG CAG CAC TAC GAG CTC ATC GGC TGG CGC CGC GCG GAC AAC GAG 1253
 Ala Arg Gln His Tyr Glu Leu Ile Gly Trp Arg Arg Ala Asp Asn Glu
 55

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 180 185 190
 CTG AAC TAC CGC CGC TTT TTC GCG GTG AAC ACG CTC GCC GGC GTC CGC 1301
 Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu Ala Gly Val Arg
 10 195 200 205
 GTG GAA ATC CCC GCC GTC TTC GAC GAG GCA CAC CAG GAG GTG GTG CGC 1349
 Val Glu Ile Pro Ala Val Phe Asp Glu Ala His Gln Glu Val Val Arg
 15 210 215 220
 TGG TTC CGC GAG GAC CTT GCG GAC GGC CTG CGG ATC GAC CAC CCG GAC 1397
 Trp Phe Arg Glu Asp Leu Ala Asp Gly Leu Arg Ile Asp His Pro Asp
 20 225 230 235 240
 GGC CTC GCT GAC CCC GAG GGG TAC CTG AAG CGA CTC CGG GAA GTC ACC 1445
 Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val Thr
 25 245 250 255
 GGC GGC GCT TAC CTG CTG ATC GAA AAG ATC CTG GAG CCG GGG GAG CAG 1493
 Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln
 30 260 265 270
 CTG CCC GCC AGC TTC GAG TGT GAA GGC ACC ACA GGC TAC GAC GCC CTC 1541
 Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu
 35 275 280 285
 GCC GAC GTC GAC CGG GTT CTC GTG GAC CCG CGC GGC CAG GAA CCG CTG 1589
 Ala Asp Val Asp Arg Val Leu Val Asp Pro Arg Gly Gln Glu Pro Leu
 40 290 295 300
 GAC CGG CTT GAC GCG TCC CTG CGT GGC GGC GAG CCC GCC GAC TAC CAG 1637
 Asp Arg Leu Asp Ala Ser Leu Arg Gly Gly Glu Pro Ala Asp Tyr Gln
 45 305 310 315 320
 GAC ATG ATC CGC GGA ACC AAG CGC CGG ATC ACC GAC GGT ATC CTG CAC 1685
 Asp Met Ile Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His
 50 325 330 335
 TCG GAG ATC CTG CGG CTG GCC CGG CTG GTT CCG GGC GAC GCC AAC GTT 1733
 55

5 Ser Glu Ile Leu Arg Leu Ala Arg Leu Val Pro Gly Asp Ala Asn Val
 340 345 350
 TCA ATC GAC GCC GGA GCC GAC GCT CTC GCC GAA ATC ATC GCC GCC TTC 1781
 10 Ser Ile Asp Ala Gly Ala Asp Ala Leu Ala Glu Ile Ile Ala Ala Phe
 355 360 365
 CCG GTC TAC CGC ACC TAC CTG CCG GAG GGC GCC GAG GTC CTG AAG GAG 1829
 15 Pro Val Tyr Arg Thr Tyr Leu Pro Glu Gly Ala Glu Val Leu Lys Glu
 370 375 380
 GCG TGC GAG CTT GCC GCG CGT AGG CGG CCG GAA CTC GAC CAG GCC ATC 1877
 20 Ala Cys Glu Leu Ala Ala Arg Arg Arg Pro Glu Leu Asp Gln Ala Ile
 385 390 395 400
 CAG GCT CTG CAG CCG CTG CTG CTG GAC ACG GAC CTC GAG CTT GCC CGG 1925
 25 Gln Ala Leu Gln Pro Leu Leu Leu Asp Thr Asp Leu Glu Leu Ala Arg
 405 410 415
 CGC TTC CAG CAG ACC TCG GGC ATG GTC ATG GCC AAG GGC GTG GAG GAC 1973
 30 Arg Phe Gln Gln Thr Ser Gly Met Val Met Ala Lys Gly Val Glu Asp
 420 425 430
 ACC GCG TTC TTC CGC TAC AAC CGC CTG GGC ACC CTC ACG GAA GTG GGC 2021
 35 Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly Thr Leu Thr Glu Val Gly
 435 440 445
 GCC GAC CCC ACC GAG TTC GCC GTG GAG CCG GAC GAG TTC CAC GCC CGG 2069
 40 Ala Asp Pro Thr Glu Phe Ala Val Glu Pro Asp Glu Phe His Ala Arg
 450 455 460
 CTG GCA CGC CGG CAG GCC GAG CTT CCG CTG TCC ATG ACG ACG CTG AGC 2117
 45 Leu Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met Thr Thr Leu Ser
 465 470 475 480
 ACG CAC GAC ACC AAG CGC AGC GAG GAC ACC CGA GCA AGG ATT TCG GTC 2165
 50 Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg Ile Ser Val
 485 490 495

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5 645 650 655
 TCA TTT ACC GAT GAG CGG ACG AAG CTG CTA GTG ACG TCG CGC GCG CTG 2693
 Ser Phe Thr Asp Glu Arg Thr Lys Leu Leu Val Thr Ser Arg Ala Leu
 10 660 665 670
 CGG CTG CGC CGG GAC CGT CCG GAG CTG TTC ACG GGG TAC CGG CCG GTC 2741
 Arg Leu Arg Arg Asp Arg Pro Glu Leu Phe Thr Gly Tyr Arg Pro Val
 15 675 680 685
 CTG GCC AGC GGG CCC GCC GCC GGG CAC CTG CTC GCG TTC GAC CGC GGC 2789
 Leu Ala Ser Gly Pro Ala Ala Gly His Leu Leu Ala Phe Asp Arg Gly
 20 690 695 700
 ACC GCG GCG GCG CCG GGT GCA TTG ACC CTC GCC ACG CGG CTT CCC TAC 2837
 Thr Ala Ala Ala Pro Gly Ala Leu Thr Leu Ala Thr Arg Leu Pro Tyr
 25 705 710 715 720
 GGG CTG GAA CAG TCG GGT GGA TGG CGG GAC ACC GCC GTC GAA CTT AAC 2885
 Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr Ala Val Glu Leu Asn
 30 725 730 735
 ACC GCC ATG AAA GAC GAA CTG ACC GGT GCC GGC TTC GGA CCG GGG GCA 2933
 Thr Ala Met Lys Asp Glu Leu Thr Gly Ala Gly Phe Gly Pro Gly Ala
 35 740 745 750
 GTG AAG ATC GCC GAC ATC TTC CGG TCG TTC CCC GTT GCG CTG CTG GTG 2981
 Val Lys Ile Ala Asp Ile Phe Arg Ser Phe Pro Val Ala Leu Leu Val
 40 755 760 765
 CCG CAG ACA GGA GGA GAG TCA 3002
 Pro Gln Thr Gly Gly Glu Ser
 45 770 775
 TGACGCACAC CTACCCGCGG GAAGCCGCGA AACCCGTCCT GGGCCCCGCA CGCTACGACG 3062
 50 TCTGGGCGCC C 3073

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22. The transformant as claimed in claim 16, wherein said DNA is derived from a microorganism selected from the group consisting of the genera *Rhizobium*, *Arthrobacter*, *Brevibacterium*, *Flavobacterium*, *Micrococcus*, *Curtobacterium*, *Mycobacterium* and *Terrabacter*.

23. The transformant as claimed in claim 16, wherein said self-replicable vector is a plasmid vector Bluescript II SK(+).
24. The transformant as claimed in claim 16, wherein said host is a microorganism of the species *Escherichia coli*.
25. A recombinant enzyme which forms a non-reducing saccharide having trehalose structure as an end unit from a reducing amylaceous saccharide having a degree of glucose polymerization of 3 or higher.
26. The recombinant enzyme as claimed in claim 25, which has the following physicochemical properties:
 (1) Molecular weight
 About 76,000-87,000 daltons on sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE); and
 (2) Isoelectric point (pI)
 About 3.6-4.6 on isoelectrophoresis.
27. The recombinant enzyme as claimed in claim 25, which has an amino acid sequence selected from the group consisting of those as shown in the following SEQ ID NOs:2 and 4 that initiate from the N-terminal, and homologous amino acid sequences to these amino acid sequences:

SEQ ID NO:2

Met Arg Thr Pro Ala Ser Thr Tyr Arg Leu Gln Ile Arg Arg Gly Phe Thr

1 5 10 15

Leu Phe Asp Ala Ala Glu Thr Val Pro Tyr Leu Lys Ser Leu Gly Val Asp

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 20 25 30
 Trp Ile Tyr Leu Ser Pro Ile Leu Lys Ala Glu Ser Gly Ser Asp His Gly
 10 35 40 45 50
 Tyr Asp Val Thr Asp Pro Ala Val Val Asp Pro Glu Arg Gly Gly Pro Glu
 55 60 65
 15 Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Gly Ala Gly Met Gly Val Leu
 70 75 80 85
 Ile Asp Ile Val Pro Asn His Val Gly Val Ala Ser Pro Pro Gln Asn Pro
 90 95 100
 20 Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg Gly Ser Pro Tyr Ala Val Ala
 105 110 115
 25 Phe Asp Val Asp Trp Asp Leu Ala Gly Gly Arg Ile Arg Ile Pro Val Leu
 120 125 130 135
 Gly Ser Asp Asp Asp Leu Asp Gln Leu Glu Ile Lys Asp Gly Glu Leu Arg
 140 145 150
 30 Tyr Tyr Asp His Arg Phe Pro Leu Ala Glu Gly Ser Tyr Arg Asp Gly Asp
 155 160 165 170
 35 Ser Pro Gln Asp Val His Gly Arg Gln His Tyr Glu Leu Ile Gly Trp Arg
 175 180 185
 Arg Ala Asp Asn Glu Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu
 190 195 200
 40 Ala Gly Ile Arg Val Glu Val Pro Pro Val Phe Asp Glu Ala His Gln Glu
 205 210 215 220
 45 Val Val Arg Trp Phe Arg Ala Gly Leu Ala Asp Gly Leu Arg Ile Asp His
 225 230 235
 Pro Asp Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val
 240 245 250 255
 50 Thr Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln
 260 265 270
 55

5 Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu Ala
 275 280 285
 10 Asp Val Asp Arg Val Phe Val Asp Pro Arg Gly Gln Val Pro Leu Asp Arg
 290 295 300 305
 Leu Asp Ala Arg Leu Arg Gly Gly Ala Pro Ala Asp Tyr Glu Asp Met Ile
 310 315 320
 15 Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His Ser Glu Ile Leu
 325 330 335 340
 20 Arg Leu Ala Arg Leu Val Pro Glu Gln Thr Gly Ile Pro Gly Glu Ala Ala
 345 350 355
 Ala Asp Ala Ile Ala Glu Ile Ile Ala Ala Phe Pro Val Tyr Arg Ser Tyr
 360 365 370
 25 Leu Pro Glu Gly Ala Glu Ile Leu Lys Glu Ala Cys Asp Leu Ala Ala Arg
 375 380 385 390
 30 Arg Arg Pro Glu Leu Gly Gln Thr Val Gln Leu Leu Gln Pro Leu Leu Leu
 395 400 405
 Asp Thr Asp Leu Glu Ile Ser Arg Arg Phe Gln Gln Thr Ser Gly Met Val
 410 415 420 425
 35 Met Ala Lys Gly Val Glu Asp Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly
 430 435 440
 40 Thr Leu Thr Glu Val Gly Ala Asp Pro Thr Glu Phe Ser Leu Glu Pro Glu
 445 450 455
 Glu Phe His Val Arg Met Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met
 460 465 470 475
 45 Thr Thr Leu Ser Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg
 480 485 490
 50 Ile Ser Val Ile Ala Glu Val Ala Pro Glu Trp Glu Lys Ala Leu Asp Arg
 495 500 505 510
 Leu Asn Thr Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Thr Leu Leu Trp

5 515 520 525
 Gln Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Ser Tyr
 530 535 540
 10 Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Ser Trp Thr Asp Pro
 545 550 555 560
 Asp Pro Ala Phe Glu Glu Ala Leu Ser Ala Val Val Asp Ser Ala Phe Asp
 15 565 570 575
 Asn Pro Glu Val Arg Ala Glu Leu Glu Ala Leu Val Gly Leu Leu Ala Pro
 580 585 590 595
 20 His Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln Leu Thr Met Pro
 600 605 610
 Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp Asp Arg Ser Leu Thr
 25 615 620 625
 Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Ala Glu Arg Ile Arg Ala Leu
 630 635 640 645
 30 Asp Gln Leu Asp Ala Gly His Arg Pro Asp Ser Phe Gln Asp Glu Ala Val
 650 655 660
 Lys Leu Leu Val Thr Ser Arg Ala Leu Arg Leu Arg Arg Asn Arg Pro Glu
 35 665 670 675 680
 Leu Phe Thr Gly Tyr Arg Pro Val His Ala Arg Gly Pro Ala Ala Gly His
 685 690 695
 40 Leu Val Ala Phe Asp Arg Gly Ala Gly Gly Val Leu Ala Leu Ala Thr Arg
 700 705 710
 Leu Pro Tyr Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr Ala Val Glu
 45 715 720 725 730
 Leu Glu Ala Ala Met Thr Asp Glu Leu Thr Gly Ser Thr Phe Gly Pro Gly
 735 740 745
 50 Pro Ala Ala Leu Ser Glu Val Phe Arg Ala Tyr Pro Val Ala Leu Leu Val
 750 755 760 765
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Pro Ala Thr Gly Gly Lys Ser

770

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SEQ ID NO:4

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Met Arg Thr Pro Val Ser Thr Tyr Arg Leu Gln Ile Arg Lys Gly Phe Thr

1 5 10 15

Leu Phe Asp Ala Ala Lys Thr Val Pro Tyr Leu His Ser Leu Gly Val Asp

20 25 30

Trp Val Tyr Leu Ser Pro Val Leu Thr Ala Glu Gln Gly Ser Asp His Gly

35 40 45 50

Tyr Asp Val Thr Asp Pro Ser Ala Val Asp Pro Glu Arg Gly Gly Pro Glu

55 60 65

Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Ala Ala Gly Met Gly Val Leu

70 75 80 85

Ile Asp Ile Val Pro Asn His Val Gly Val Ala Thr Pro Ala Gln Asn Pro

90 95 100

Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg Gln Ser Arg Tyr Ala Glu Ala

105 110 115

Phe Asp Val Asp Trp Asp Leu Ala Gly Gly Arg Ile Arg Leu Pro Val Leu

120 125 130 135

Gly Ser Asp Asp Asp Leu Asp Gln Leu Glu Ile Arg Asp Gly Glu Leu Arg

140 145 150

Tyr Tyr Asp His Arg Phe Pro Leu Ala Glu Gly Thr Tyr Ala Glu Gly Asp

155 160 165 170

Ala Pro Arg Asp Val His Ala Arg Gln His Tyr Glu Leu Ile Gly Trp Arg

175 180 185

Arg Ala Asp Asn Glu Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu

190 195 200

Ala Gly Val Arg Val Glu Ile Pro Ala Val Phe Asp Glu Ala His Gln Glu

5
 205 210 215 220
 Val Val Arg Trp Phe Arg Glu Asp Leu Ala Asp Gly Leu Arg Ile Asp His
 10 225 230 235
 Pro Asp Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val
 240 245 250 255
 15 Thr Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln
 260 265 270
 Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu Ala
 20 275 280 285
 Asp Val Asp Arg Val Leu Val Asp Pro Arg Gly Gln Glu Pro Leu Asp Arg
 290 295 300 305
 25 Leu Asp Ala Ser Leu Arg Gly Gly Glu Pro Ala Asp Tyr Gln Asp Met Ile
 310 315 320
 Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His Ser Glu Ile Leu
 30 325 330 335 340
 Arg Leu Ala Arg Leu Val Pro Gly Asp Ala Asn Val Ser Ile Asp Ala Gly
 345 350 355
 35 Ala Asp Ala Leu Ala Glu Ile Ile Ala Ala Phe Pro Val Tyr Arg Thr Tyr
 360 365 370
 Leu Pro Glu Gly Ala Glu Val Leu Lys Glu Ala Cys Glu Leu Ala Ala Arg
 40 375 380 385 390
 Arg Arg Pro Glu Leu Asp Gln Ala Ile Gln Ala Leu Gln Pro Leu Leu Leu
 395 400 405
 45 Asp Thr Asp Leu Glu Leu Ala Arg Arg Phe Gln Gln Thr Ser Gly Met Val
 410 415 420 425
 Met Ala Lys Gly Val Glu Asp Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly
 50 430 435 440
 Thr Leu Thr Glu Val Gly Ala Asp Pro Thr Glu Phe Ala Val Glu Pro Asp
 445 450 455

55

5 Glu Phe His Ala Arg Leu Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met
 460 465 470 475
 10 Thr Thr Leu Ser Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg
 480 485 490
 Ile Ser Val Ile Ser Glu Val Ala Gly Asp Trp Glu Lys Ala Leu Asn Arg
 495 500 505 510
 15 Leu Arg Asp Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Ala Leu Leu Trp
 515 520 525
 20 Gln Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Tyr Tyr
 530 535 540
 Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Asn Trp Thr Asp Pro
 545 550 555 560
 25 Ala Pro Ala Phe Glu Glu Lys Leu Lys Ala Ala Val Asp Ala Val Phe Asp
 565 570 575
 30 Asn Pro Ala Val Gln Ala Glu Val Glu Ala Leu Val Glu Leu Leu Glu Pro
 580 585 590 595
 Tyr Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln Leu Thr Met Pro
 600 605 610
 35 Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp Asp Arg Ser Leu Thr
 615 620 625
 40 Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Asp Asp Arg Arg Ala Ala Leu
 630 635 640 645
 Glu Gln Leu Asp Ala Gly Asp Leu Pro Ala Ser Phe Thr Asp Glu Arg Thr
 650 655 660
 45 Lys Leu Leu Val Thr Ser Arg Ala Leu Arg Leu Arg Arg Asp Arg Pro Glu
 665 670 675 680
 50 Leu Phe Thr Gly Tyr Arg Pro Val Leu Ala Ser Gly Pro Ala Ala Gly His
 685 690 695
 Leu Leu Ala Phe Asp Arg Gly Thr Ala Ala Ala Pro Gly Ala Leu Thr Leu

55

	700	705	710
5	Ala Thr Arg Leu Pro Tyr Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr		
	715	720	725 730
	Ala Val Glu Leu Asn Thr Ala Met Lys Asp Glu Leu Thr Gly Ala Gly Phe		
10	735	740	745
	Gly Pro Gly Ala Val Lys Ile Ala Asp Ile Phe Arg Ser Phe Pro Val Ala		
	750	755	760 765
15	Leu Leu Val Pro Gln Thr Gly Gly Glu Ser		
	770	775	

- 20 28. A process for producing a recombinant enzyme, which comprises culturing a transformant capable of forming the recombinant enzyme of claim 25, and collecting the recombinant enzyme from the resultant culture.
- 25 29. The process as claimed in claim 28, wherein said recombinant enzyme has the following physicochemical properties:
- (1) Molecular weight
About 76,000-87,000 daltons on sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE); and
- (2) Isoelectric point (pI)
About 3.6-4.6 on isoelectrophoresis.
- 30 30. The process of as claimed in claim 28, wherein said recombinant enzyme has an amino acid sequence selected from the group consisting of those as shown in SEQ ID NOs:2 and 4 that initiate from the N-terminal, and homologous amino acid sequences to these amino acid sequences:

35 SEQ ID NO:2

	Met Arg Thr Pro Ala Ser Thr Tyr Arg Leu Gln Ile Arg Arg Gly Phe Thr
40	1 5 10 15

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5 Leu Phe Asp Ala Ala Glu Thr Val Pro Tyr Leu Lys Ser Leu Gly Val Asp
 20 25 30
 Trp Ile Tyr Leu Ser Pro Ile Leu Lys Ala Glu Ser Gly Ser Asp His Gly
 10 35 40 45 50
 Tyr Asp Val Thr Asp Pro Ala Val Val Asp Pro Glu Arg Gly Gly Pro Glu
 55 60 65
 15 Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Gly Ala Gly Met Gly Val Leu
 70 75 80 85
 Ile Asp Ile Val Pro Asn His Val Gly Val Ala Ser Pro Pro Gln Asn Pro
 20 90 95 100
 Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg Gly Ser Pro Tyr Ala Val Ala
 105 110 115
 25 Phe Asp Val Asp Trp Asp Leu Ala Gly Gly Arg Ile Arg Ile Pro Val Leu
 120 125 130 135
 Gly Ser Asp Asp Asp Leu Asp Gln Leu Glu Ile Lys Asp Gly Glu Leu Arg
 30 140 145 150
 Tyr Tyr Asp His Arg Phe Pro Leu Ala Glu Gly Ser Tyr Arg Asp Gly Asp
 155 160 165 170
 35 Ser Pro Gln Asp Val His Gly Arg Gln His Tyr Glu Leu Ile Gly Trp Arg
 175 180 185
 Arg Ala Asp Asn Glu Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu
 40 190 195 200
 Ala Gly Ile Arg Val Glu Val Pro Pro Val Phe Asp Glu Ala His Gln Glu
 205 210 215 220
 45 Val Val Arg Trp Phe Arg Ala Gly Leu Ala Asp Gly Leu Arg Ile Asp His
 225 230 235
 Pro Asp Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val
 50 240 245 250 255
 Thr Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln
 55

5 260 265 270
 Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu Ala
 275 280 285
 10 Asp Val Asp Arg Val Phe Val Asp Pro Arg Gly Gln Val Pro Leu Asp Arg
 290 295 300 305
 Leu Asp Ala Arg Leu Arg Gly Gly Ala Pro Ala Asp Tyr Glu Asp Met Ile
 15 310 315 320
 Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His Ser Glu Ile Leu
 325 330 335 340
 20 Arg Leu Ala Arg Leu Val Pro Glu Gln Thr Gly Ile Pro Gly Glu Ala Ala
 345 350 355
 Ala Asp Ala Ile Ala Glu Ile Ile Ala Ala Phe Pro Val Tyr Arg Ser Tyr
 25 360 365 370
 Leu Pro Glu Gly Ala Glu Ile Leu Lys Glu Ala Cys Asp Leu Ala Ala Arg
 375 380 385 390
 30 Arg Arg Pro Glu Leu Gly Gln Thr Val Gln Leu Leu Gln Pro Leu Leu Leu
 395 400 405
 Asp Thr Asp Leu Glu Ile Ser Arg Arg Phe Gln Gln Thr Ser Gly Met Val
 35 410 415 420 425
 Met Ala Lys Gly Val Glu Asp Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly
 430 435 440
 40 Thr Leu Thr Glu Val Gly Ala Asp Pro Thr Glu Phe Ser Leu Glu Pro Glu
 445 450 455
 Glu Phe His Val Arg Met Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met
 45 460 465 470 475
 Thr Thr Leu Ser Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg
 480 485 490
 50 Ile Ser Val Ile Ala Glu Val Ala Pro Glu Trp Glu Lys Ala Leu Asp Arg
 495 500 505 510
 55

5	Leu	Asn	Thr	Leu	Ala	Pro	Leu	Pro	Asp	Gly	Pro	Leu	Ser	Thr	Leu	Leu	Trp
						515					520					525	
	Gln	Ala	Ile	Ala	Gly	Ala	Trp	Pro	Ala	Ser	Arg	Glu	Arg	Leu	Gln	Ser	Tyr
10						530					535				540		
	Ala	Leu	Lys	Ala	Ala	Arg	Glu	Ala	Gly	Asn	Ser	Thr	Ser	Trp	Thr	Asp	Pro
	545					550					555					560	
15	Asp	Pro	Ala	Phe	Glu	Glu	Ala	Leu	Ser	Ala	Val	Val	Asp	Ser	Ala	Phe	Asp
						565					570				575		
	Asn	Pro	Glu	Val	Arg	Ala	Glu	Leu	Glu	Ala	Leu	Val	Gly	Leu	Leu	Ala	Pro
20						580					585				590		595
	His	Gly	Ala	Ser	Asn	Ser	Leu	Ala	Ala	Lys	Leu	Val	Gln	Leu	Thr	Met	Pro
						600					605				610		
25	Gly	Val	Pro	Asp	Val	Tyr	Gln	Gly	Thr	Glu	Phe	Trp	Asp	Arg	Ser	Leu	Thr
						615					620				625		
	Asp	Pro	Asp	Asn	Arg	Arg	Pro	Phe	Ser	Phe	Ala	Glu	Arg	Ile	Arg	Ala	Leu
30						630					635				640		645
	Asp	Gln	Leu	Asp	Ala	Gly	His	Arg	Pro	Asp	Ser	Phe	Gln	Asp	Glu	Ala	Val
						650					655				660		
35	Lys	Leu	Leu	Val	Thr	Ser	Arg	Ala	Leu	Arg	Leu	Arg	Arg	Asn	Arg	Pro	Glu
						665					670				675		680
	Leu	Phe	Thr	Gly	Tyr	Arg	Pro	Val	His	Ala	Arg	Gly	Pro	Ala	Ala	Gly	His
40						685					690				695		
	Leu	Val	Ala	Phe	Asp	Arg	Gly	Ala	Gly	Gly	Val	Leu	Ala	Leu	Ala	Thr	Arg
						700					705				710		
45	Leu	Pro	Tyr	Gly	Leu	Glu	Gln	Ser	Gly	Gly	Trp	Arg	Asp	Thr	Ala	Val	Glu
						715					720				725		730
	Leu	Glu	Ala	Ala	Met	Thr	Asp	Glu	Leu	Thr	Gly	Ser	Thr	Phe	Gly	Pro	Gly
50						735					740				745		
	Pro	Ala	Ala	Leu	Ser	Glu	Val	Phe	Arg	Ala	Tyr	Pro	Val	Ala	Leu	Leu	Val

750 755 760 765

Pro Ala Thr Gly Gly Lys Ser

5 770

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SEQ ID NO:4

15 Met Arg Thr Pro Val Ser Thr Tyr Arg Leu Gln Ile Arg Lys Gly Phe Thr

1 5 10 15

Leu Phe Asp Ala Ala Lys Thr Val Pro Tyr Leu His Ser Leu Gly Val Asp

20 20 25 30

Trp Val Tyr Leu Ser Pro Val Leu Thr Ala Glu Gln Gly Ser Asp His Gly

35 40 45 50

25 Tyr Asp Val Thr Asp Pro Ser Ala Val Asp Pro Glu Arg Gly Gly Pro Glu

55 60 65

Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Ala Ala Gly Met Gly Val Leu

30 70 75 80 85

Ile Asp Ile Val Pro Asn His Val Gly Val Ala Thr Pro Ala Gln Asn Pro

90 95 100

35 Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg Gln Ser Arg Tyr Ala Glu Ala

105 110 115

Phe Asp Val Asp Trp Asp Leu Ala Gly Gly Arg Ile Arg Leu Pro Val Leu

40 120 125 130 135

Gly Ser Asp Asp Asp Leu Asp Gln Leu Glu Ile Arg Asp Gly Glu Leu Arg

140 145 150

45 Tyr Tyr Asp His Arg Phe Pro Leu Ala Glu Gly Thr Tyr Ala Glu Gly Asp

155 160 165 170

50 Ala Pro Arg Asp Val His Ala Arg Gln His Tyr Glu Leu Ile Gly Trp Arg

175 180 185

Arg Ala Asp Asn Glu Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu

190 195 200

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5 Ala Gly Val Arg Val Glu Ile Pro Ala Val Phe Asp Glu Ala His Gln Glu
 205 210 215 220
 10 Val Val Arg Trp Phe Arg Glu Asp Leu Ala Asp Gly Leu Arg Ile Asp His
 225 230 235
 Pro Asp Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val
 15 240 245 250 255
 Thr Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln
 260 265 270
 20 Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu Ala
 275 280 285
 Asp Val Asp Arg Val Leu Val Asp Pro Arg Gly Gln Glu Pro Leu Asp Arg
 25 290 295 300 305
 Leu Asp Ala Ser Leu Arg Gly Gly Glu Pro Ala Asp Tyr Gln Asp Met Ile
 310 315 320
 30 Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His Ser Glu Ile Leu
 325 330 335 340
 Arg Leu Ala Arg Leu Val Pro Gly Asp Ala Asn Val Ser Ile Asp Ala Gly
 35 345 350 355
 Ala Asp Ala Leu Ala Glu Ile Ile Ala Ala Phe Pro Val Tyr Arg Thr Tyr
 360 365 370
 40 Leu Pro Glu Gly Ala Glu Val Leu Lys Glu Ala Cys Glu Leu Ala Ala Arg
 375 380 385 390
 Arg Arg Pro Glu Leu Asp Gln Ala Ile Gln Ala Leu Gln Pro Leu Leu Leu
 45 395 400 405
 Asp Thr Asp Leu Glu Leu Ala Arg Arg Phe Gln Gln Thr Ser Gly Met Val
 410 415 420 425
 50 Met Ala Lys Gly Val Glu Asp Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly
 430 435 440
 Thr Leu Thr Glu Val Gly Ala Asp Pro Thr Glu Phe Ala Val Glu Pro Asp

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5 445 450 455
 Glu Phe His Ala Arg Leu Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met
 460 465 470 475
 10 Thr Thr Leu Ser Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg
 480 485 490
 Ile Ser Val Ile Ser Glu Val Ala Gly Asp Trp Glu Lys Ala Leu Asn Arg
 15 495 500 505 510
 Leu Arg Asp Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Ala Leu Leu Trp
 515 520 525
 20 Gln Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Tyr Tyr
 530 535 540
 Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Asn Trp Thr Asp Pro
 25 545 550 555 560
 Ala Pro Ala Phe Glu Glu Lys Leu Lys Ala Ala Val Asp Ala Val Phe Asp
 565 570 575
 30 Asn Pro Ala Val Gln Ala Glu Val Glu Ala Leu Val Glu Leu Leu Glu Pro
 580 585 590 595
 Tyr Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln Leu Thr Met Pro
 35 600 605 610
 Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp Asp Arg Ser Leu Thr
 615 620 625
 40 Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Asp Asp Arg Arg Ala Ala Leu
 630 635 640 645
 45 Glu Gln Leu Asp Ala Gly Asp Leu Pro Ala Ser Phe Thr Asp Glu Arg Thr
 650 655 660
 Lys Leu Leu Val Thr Ser Arg Ala Leu Arg Leu Arg Arg Asp Arg Pro Glu
 50 665 670 675 680
 Leu Phe Thr Gly Tyr Arg Pro Val Leu Ala Ser Gly Pro Ala Ala Gly His
 685 690 695

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Leu Leu Ala Phe Asp Arg Gly Thr Ala Ala Ala Pro Gly Ala Leu Thr Leu

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Ala Thr Arg Leu Pro Tyr Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr

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Ala Val Glu Leu Asn Thr Ala Met Lys Asp Glu Leu Thr Gly Ala Gly Phe

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Gly Pro Gly Ala Val Lys Ile Ala Asp Ile Phe Arg Ser Phe Pro Val Ala

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Leu Leu Val Pro Gln Thr Gly Gly Glu Ser

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31. The process as claimed in claim 28, wherein said transformant is obtained by introducing into a suitable host a recombinant DNA containing a self-replicable vector and a DNA encoding an enzyme which forms a non-reducing saccharide having trehalose structure as an end unit from a reducing amylose saccharide having a degree of glucose polymerization of 3 or higher.

25

32. The process as claimed in claim 28, wherein said DNA has a base sequence selected from the group consisting of those as shown in SEQ ID NOs:1 and 3 that initiate from the 5'-terminus, homologous base sequences to the base sequences, and complementary base sequence to these base sequences:

30

SEQ ID NO:1

35

ATGAGGACAC CCGCCTCGAC CTACCGGCTG CAGATCAGGC GGGGTTTCAC GCTGTTTGAT 60

GCCGCCGAGA CCGTGCCCTA CCTGAAGTCA CTCGGGGTGG ACTGGATCTA CCTGTCGCCC 120

ATCCTGAAGG CAGAGAGCGG CTCCGACCAC GGCTATGACG TCACCGATCC CGCCGTAGTG 180

40

GACCCGGAGC GCGGCGGCCC TGAAGGGCTG GCCGCGGTGT CCAAGGCGGC CCGCGGTGCC 240

GGCATGGGCG TGCTGATCGA CATCGTGCCG AACCACGTGG GCGTGGCGTC GCCGCCGAG 300

AACCCGTGGT GGTGGTCGCT GCTCAAGGAA GGGCGCGGGT CGCCCTACGC CGTGGCGTTC 360

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50

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5 GACGTCGACT GGGACCTGGC GGGGGGCCGC ATCCGGATCC CCGTCCTGGG CAGCGACGAC 420
 GATCTGGACC AGCTCGAAAT CAAGGACGGC GAGCTGCGGT ACTACGACCA CCGCTTCCCG 480
 CTGGCCGAGG GCAGCTACCG GGACGGCGAC TCCCCGAGG ACGTCCACGG CCGGCAGCAC 540
 10 TACGAACTCA TCGGCTGGCG GCGCGCCGAC AATGAACTGA ACTACCGCCG GTTCTTCGCG 600
 GTGAACACGC TCGCCGGCAT CCGGGTGGAG GTGCCGCCGG TCTTCGATGA AGCGCACCAG 660
 GAGGTGGTGC GCTGGTTCCG TCGGGGGCTC GCCGACGGGC TCGGATCGA CCACCCGGAC 720
 15 GGCCTGGCCG ATCCCGAGGG GTATTTGAAG CGGCTCCGTG AGGTCACCGG GGGCGCGTAC 780
 CTGCTCATCG AAAAGATCCT CGAGCCGGGC GAACAGTTGC CGGCCAGCTT CGAGTGCGAA 840
 GGCACCACCG GCTACGACGC CCTCGCGGAT GTCGACAGGG TCTTCGTGGA CCCGCGGGGA 900
 20 CAGGTGCCGC TGGACCGTCT GGACGCACGG CTGCGCGGCG GTGCGCCGGC CGACTACGAG 960
 GACATGATCC GCGGGACCAA GCGCCGGATC ACCGACGGCA TCCTGCACTC CGAGATCCTG 1020
 CGCCTTGCCA GGCTGGTGCC CGAGCAGACC GGAATTCCCG GGGAGGCGGC CGCGGATGCG 1080
 25 ATCGCGGAGA TCATCGCGGC CTTCCCGGTC TACCGGTCCT ATCTTCCCGA GGGCGCGGAG 1140
 ATCCTGAAGG AGGCCTGCGA CCTCGCCGCG CGGAGGCGTC CGGAACTGGG CCAGACCGTC 1200
 CAGCTGCTGC AGCCGCTGCT GCTGGATACC GACCTCGAGA TTTCCCGCAG GTTCCAGCAG 1260
 30 ACCTCGGGAA TGGTCATGGC CAAAGGCGTG GAGGACACCG CGTTCTTCCG CTACAACCGG 1320
 CTGGGAACGC TCACCGAGGT GGGCGCCGAC CCCACCGAGT TCTCGCTGGA ACCGGAGGAG 1380
 TTTACGTCC GGATGGCCCG CCGGCAGGCC GAACTCCCGC TCTCCATGAC CACCCTGAGC 1440
 35 ACGCACGACA CCAAGCGCAG CGAGGACACC CGGGCCCGGA TCTCGGTGAT CGCCGAGGTC 1500
 GCGCCTGAAT GGGAAAAGGC CCTGGACAGG CTGAACACCC TCGCTCCGCT GCCGGACGGC 1560
 CCGCTCTCCA CGCTGCTCTG GCAGGCGATT GCGGGGGCAT GGCCGGCCAG CCGGGAACGC 1620
 40 CTTCAGTCCT ACGCCCTGAA AGCGGCGCGC GAAGCCGGGA ACTCGACCAG CTGGACCGAT 1680
 CCGGACCCGG CATTGAGGA GGCACCTTCC GCCGTGTCG ACTCCGCTT CGACAATCCG 1740
 GAGGTGCGTG CGGAACTTGA GGCCCTGGTG GGCCTCCTTG CGCCGCACGG TCGTCCAAC 1800
 45 TCGCTCGCGG CAAAGCTTGT CCAGCTGACC ATGCCGGGCG TTCCGGACGT GTACCAGGGC 1860
 ACCGATTTCT GGGACAGGTC GCTGACCGAT CCGGACAACC GGCGCCCTT CAGCTTCGCC 1920
 50 GAACGGATTA GGGCCTTGGA CCAGTTGGAC GCCGGCCACC GTCCGGACTC CTTCCAGGAC 1980
 GAGGCGGTCA AGCTGCTGGT CACCTCGAGG GCGCTGCGGC TCGGCGGAA CCGGCCCGAG 2040
 CTCTTACCG GCTACCGCCC CGTGATGCC AGGGGCCCCG CCGCCGGGCA CCTGGTGGCG 2100

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TTCGACCGCG GCGCCGGGGG AGTGCTGGCG CTTGCCACCC GGCTCCCCTA CGGGCTGGAA 2160
 CAGTCGGGCG GCTGGCGGGA CACCGCCGTC GAGCTTGAAG CCGCCATGAC GGACGAACTG 2220
 5 ACCGGCTCCA CTTTCGGGCC GGGACCGGCG GCGCTGTCAG AAGTCTTCCG GGCCTACCEG 2280
 GTGGCCTTGT TGGTCCCCGC GACAGGAGGC AAGTCA 2316

SEQ ID NO:3

ATGAGAACGC CAGTCTCCAC GTACAGGCTG CAGATCAGGA AGGGATTCAC ACTCTTCGAC 60
 GCGGCCAAAA CCGTTCGTA CCTGCACTCG CTCGGCGTCG ACTGGGTCTA CCTTTETCCG 120
 20 GTCCTGACTG CCGAGCAGGG CTCGACCAC GGGTACGACG TCACCGATCC CTCGCCGTCG 180
 GACCCCGAAC GCGGCGGGCC GGAGGGCCTC GCGGCGGTTT CCAAGGCGGC CCGCGCCGCG 240
 GGCATGGGCG TGCTGATCGA CATCGTGCCC AACCACGTGG GCGTCGCGAC GCCGGCGCAG 300
 25 AACCCTGGT GGTGGTCGCT GCTCAAGGAG GGACGCCAGT CCCGTTACGC GGAGGCGTTC 360
 GACGTCGATT GGGACCTCGC CGGGGGACGC ATCCGGCTGC CGGTGCTCGG CAGCGACGAT 420
 GACCTCGACC AGCTCGAAAT CAGGGACGGG GAGCTGCGGT ACTACGACCA CCGATTCCCG 480
 30 CTCGCCGAGG GAACCTACGC CGAAGGCGAC GCGCCGCGGG ATGTCCACGC CCGGCAGCAC 540
 TACGAGCTCA TCGGCTGGCG CCGCGCGGAC AACGAGCTGA ACTACCGCCG CTTTTTCGCG 600
 GTGAACACGC TCGCCGGCGT CCGCGTGGAA ATCCCGCCG TCTTCGACGA GGCACACCAG 660
 35 GAGGTGGTGC GCTGGTTCCG CGAGGACCTT GCGGACGGCC TGCGGATCGA CCACCGGAC 720
 GGCCTCGCTG ACCCGGAGGG GTACCTGAAG CGACTCCGGG AAGTCACCGG CGGCGCTTAC 780
 CTGCTGATCG AAAAGATCCT GGAGCCGGGG GAGCAGCTGC CCGCCAGCTT CGAGTGTGAA 840
 40 GGCACCACAG GCTACGACGC CCTCGCCGAC GTCGACCGGG TTCTCGTGGA CCCGCGCGGC 900
 CAGGAACCGC TGGACCGGCT TGACGCGTCC CTGCGTGGCG GCGAGCCCGC CGACTACCAG 960
 GACATGATCC GCGGAACCAA GCGCCGGATC ACCGACGGTA TCCTGCACTC GGAGATCCTG 1020
 45 CGGCTGGCCC GGCTGGTTCC GGGCGACGCC AACGTTTCAA TCGACGCCGG AGCCGACGCT 1080
 CTCGCCGAAA TCATCGCCGC CTTCCCGGTC TACCGCACCT ACCTGCCGGA GGGCGCCGAG 1140
 GTCCTGAAGG AGGCGTGCGA GCTTGCCGCG CGTAGGCGGC CGGAACTCGA CCAGGCCATC 1200
 50 CAGGCTCTGC AGCCGCTGCT GCTGGACACG GACCTCGAGC TTGCCCCGCG CTTCCAGCAG 1260
 ACCTCGGGCA TGGTCATGGC CAAGGGCGTG GAGGACACCG CGTTCTTCCG CTACAACCGC 1320
 55 CTGGGCACCC TCACGGAAGT GGGCGCCGAC CCCACCGAGT TCGCCGTGGA GCCGGACGAG 1380

TTCCACGCCC GGCTGGCAGC CCGGCAGGCC GAGCTTCCGC TGTCCATGAC GACGCTGAGC 1440
 5 ACGCACGACA CCAAGCGCAG CGAGGACACC CGAGCAAGGA TTTCGGTCAT TTCCGAGGTT 1500
 GCGGGTGACT GGGAAAAGGC CTTGAACCGG CTGCGCGACC TGGCCCCGCT GCCGGACGGC 1560
 CCGCTGTCCG CGCTGCTCTG GCAGGCCATT GCCGGCGCCT GGCCCGCCAG CCGGGAACGC 1620
 10 CTGCAGTACT ACGCGCTGAA GGCCGCGCGT GAAGCGGGGA ACTCGACCAA CTGGACCGAT 1680
 CCGGCCCCCG CGTTCGAGGA GAAGCTGAAG GCCGCGGTCTG ACGCCGTGTT CGACAATCCC 1740
 GCCGTGCAGG CCGAGGTGGA AGCCCTCGTC GAGCTCCTGG AGCCGTACGG AGCTTCGAAC 1800
 15 TCCCTCGCCG CCAAGCTCGT GCAGCTGACC ATGCCCGGCG TCCCGGACGT CTACCAGGGC 1860
 ACGGAGTTCT GGGACCGGTC GCTGACGGAC CCGGACAACC GCGGGCCGTT CAGCTTCGAC 1920
 GACCGCCCGC CCGCGCTGGA GCAGCTGGAT GCCGGCGACC TTCCCGCGTC ATTTACCGAT 1980
 20 GAGCGGACGA AGCTGCTAGT GACGTCGCGC GCGCTGCGGC TCGCCCGGGA CCGTCCGGAG 2040
 CTGTTACCGG GGTACCGGCC GGTCTGGCC AGCGGGCCCG CCGCCGGGCA CCTGCTCGCG 2100
 TTCGACCGCG GCACCGCGGC GCGCGCGGT GCATTGACCC TCGCCACGCG GCTTCCCTAC 2160
 25 GGGCTGGAAC AGTCGGGTGG ATGGCGGGAC ACCGCCGTCTG AACTTAACAC CGCCATGAAA 2220
 GACGAACTGA CCGGTGCCGG CTTCGGACCG GGGGCAGTGA AGATCGCCGA CATCTTCGGG 2280
 TCGTTCCCCG TTGCGCTGCT GGTGCCGCGC ACAGGAGGAG AGTCA 2325
 30

33. The process as claimed in claim 32, wherein said DNA has a base sequence selected from the group consisting of those as shown in SEQ ID NOs:1 and 3 wherein one or more bases are replaced with other bases by means of degeneracy of genetic code without alternating their corresponding amino acid sequences as shown in the following SEQ ID NOs:2 and 4:

40 SEQ ID NO:2
 Met Arg Thr Pro Ala Ser Thr Tyr Arg Leu Gln Ile Arg Arg Gly Phe Thr
 1 5 10 15
 45 Leu Phe Asp Ala Ala Glu Thr Val Pro Tyr Leu Lys Ser Leu Gly Val Asp
 20 25 30
 Trp Ile Tyr Leu Ser Pro Ile Leu Lys Ala Glu Ser Gly Ser Asp His Gly
 50 35 40 45 50

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5 Tyr Asp Val Thr Asp Pro Ala Val Val Asp Pro Glu Arg Gly Gly Pro Glu
 55 60 65
 Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Gly Ala Gly Met Gly Val Leu
 10 70 75 80 85
 Ile Asp Ile Val Pro Asn His Val Gly Val Ala Ser Pro Pro Gln Asn Pro
 90 95 100
 15 Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg Gly Ser Pro Tyr Ala Val Ala
 105 110 115
 Phe Asp Val Asp Trp Asp Leu Ala Gly Gly Arg Ile Arg Ile Pro Val Leu
 20 120 125 130 135
 Gly Ser Asp Asp Asp Leu Asp Gln Leu Glu Ile Lys Asp Gly Glu Leu Arg
 140 145 150
 25 Tyr Tyr Asp His Arg Phe Pro Leu Ala Glu Gly Ser Tyr Arg Asp Gly Asp
 155 160 165 170
 Ser Pro Gln Asp Val His Gly Arg Gln His Tyr Glu Leu Ile Gly Trp Arg
 30 175 180 185
 Arg Ala Asp Asn Glu Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu
 190 195 200
 35 Ala Gly Ile Arg Val Glu Val Pro Pro Val Phe Asp Glu Ala His Gln Glu
 205 210 215 220
 Val Val Arg Trp Phe Arg Ala Gly Leu Ala Asp Gly Leu Arg Ile Asp His
 40 225 230 235
 Pro Asp Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val
 240 245 250 255
 45 Thr Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln
 260 265 270
 Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu Ala
 50 275 280 285
 Asp Val Asp Arg Val Phe Val Asp Pro Arg Gly Gln Val Pro Leu Asp Arg

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5	290	295	300	305
	Leu Asp Ala Arg Leu Arg Gly Gly Ala Pro Ala Asp Tyr Glu Asp Met Ile			
	310	315	320	
10	Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His Ser Glu Ile Leu			
	325	330	335	340
	Arg Leu Ala Arg Leu Val Pro Glu Gln Thr Gly Ile Pro Gly Glu Ala Ala			
15	345	350	355	
	Ala Asp Ala Ile Ala Glu Ile Ile Ala Ala Phe Pro Val Tyr Arg Ser Tyr			
	360	365	370	
20	Leu Pro Glu Gly Ala Glu Ile Leu Lys Glu Ala Cys Asp Leu Ala Ala Arg			
	375	380	385	390
	Arg Arg Pro Glu Leu Gly Gln Thr Val Gln Leu Leu Gln Pro Leu Leu Leu			
25	395	400	405	
	Asp Thr Asp Leu Glu Ile Ser Arg Arg Phe Gln Gln Thr Ser Gly Met Val			
	410	415	420	425
30	Met Ala Lys Gly Val Glu Asp Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly			
	430	435	440	
	Thr Leu Thr Glu Val Gly Ala Asp Pro Thr Glu Phe Ser Leu Glu Pro Glu			
35	445	450	455	
	Glu Phe His Val Arg Met Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met			
	460	465	470	475
40	Thr Thr Leu Ser Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg			
	480	485	490	
	Ile Ser Val Ile Ala Glu Val Ala Pro Glu Trp Glu Lys Ala Leu Asp Arg			
45	495	500	505	510
	Leu Asn Thr Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Thr Leu Leu Trp			
	515	520	525	
50	Gln Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Ser Tyr			
	530	535	540	

5 Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Ser Trp Thr Asp Pro
 545 550 555 560
 Asp Pro Ala Phe Glu Glu Ala Leu Ser Ala Val Val Asp Ser Ala Phe Asp
 10 565 570 575
 Asn Pro Glu Val Arg Ala Glu Leu Glu Ala Leu Val Gly Leu Leu Ala Pro
 580 585 590 595
 15 His Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln Leu Thr Met Pro
 600 605 610
 Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp Asp Arg Ser Leu Thr
 20 615 620 625
 Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Ala Glu Arg Ile Arg Ala Leu
 630 635 640 645
 25 Asp Gln Leu Asp Ala Gly His Arg Pro Asp Ser Phe Gln Asp Glu Ala Val
 650 655 660
 Lys Leu Leu Val Thr Ser Arg Ala Leu Arg Leu Arg Arg Asn Arg Pro Glu
 30 665 670 675 680
 Leu Phe Thr Gly Tyr Arg Pro Val His Ala Arg Gly Pro Ala Ala Gly His
 685 690 695
 35 Leu Val Ala Phe Asp Arg Gly Ala Gly Gly Val Leu Ala Leu Ala Thr Arg
 700 705 710
 Leu Pro Tyr Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr Ala Val Glu
 40 715 720 725 730
 Leu Glu Ala Ala Met Thr Asp Glu Leu Thr Gly Ser Thr Phe Gly Pro Gly
 735 740 745
 45 Pro Ala Ala Leu Ser Glu Val Phe Arg Ala Tyr Pro Val Ala Leu Leu Val
 750 755 760 765
 50 Pro Ala Thr Gly Gly Lys Ser
 770

5 SEQ ID NO:4
 Met Arg Thr Pro Val Ser Thr Tyr Arg Leu Gln Ile Arg Lys Gly Phe Thr
 1 5 10 15
 10 Leu Phe Asp Ala Ala Lys Thr Val Pro Tyr Leu His Ser Leu Gly Val Asp
 20 25 30
 Trp Val Tyr Leu Ser Pro Val Leu Thr Ala Glu Gln Gly Ser Asp His Gly
 15 35 40 45 50
 Tyr Asp Val Thr Asp Pro Ser Ala Val Asp Pro Glu Arg Gly Gly Pro Glu
 55 60 65
 20 Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Ala Ala Gly Met Gly Val Leu
 70 75 80 85
 Ile Asp Ile Val Pro Asn His Val Gly Val Ala Thr Pro Ala Gln Asn Pro
 25 90 95 100
 Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg Gln Ser Arg Tyr Ala Glu Ala
 105 110 115
 30 Phe Asp Val Asp Trp Asp Leu Ala Gly Gly Arg Ile Arg Leu Pro Val Leu
 120 125 130 135
 Gly Ser Asp Asp Asp Leu Asp Gln Leu Glu Ile Arg Asp Gly Glu Leu Arg
 35 140 145 150
 Tyr Tyr Asp His Arg Phe Pro Leu Ala Glu Gly Thr Tyr Ala Glu Gly Asp
 155 160 165 170
 40 Ala Pro Arg Asp Val His Ala Arg Gln His Tyr Glu Leu Ile Gly Trp Arg
 175 180 185
 Arg Ala Asp Asn Glu Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu
 45 190 195 200
 Ala Gly Val Arg Val Glu Ile Pro Ala Val Phe Asp Glu Ala His Gln Glu
 205 210 215 220
 50 Val Val Arg Trp Phe Arg Glu Asp Leu Ala Asp Gly Leu Arg Ile Asp His
 225 230 235

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5 Pro Asp Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val
 240 245 250 255
 Thr Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln
 10 260 265 270
 Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu Ala
 275 280 285
 15 Asp Val Asp Arg Val Leu Val Asp Pro Arg Gly Gln Glu Pro Leu Asp Arg
 290 295 300 305
 Leu Asp Ala Ser Leu Arg Gly Gly Glu Pro Ala Asp Tyr Gln Asp Met Ile
 20 310 315 320
 Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His Ser Glu Ile Leu
 325 330 335 340
 25 Arg Leu Ala Arg Leu Val Pro Gly Asp Ala Asn Val Ser Ile Asp Ala Gly
 345 350 355
 Ala Asp Ala Leu Ala Glu Ile Ile Ala Ala Phe Pro Val Tyr Arg Thr Tyr
 30 360 365 370
 Leu Pro Glu Gly Ala Glu Val Leu Lys Glu Ala Cys Glu Leu Ala Ala Arg
 375 380 385 390
 35 Arg Arg Pro Glu Leu Asp Gln Ala Ile Gln Ala Leu Gln Pro Leu Leu Leu
 395 400 405
 Asp Thr Asp Leu Glu Leu Ala Arg Arg Phe Gln Gln Thr Ser Gly Met Val
 40 410 415 420 425
 Met Ala Lys Gly Val Glu Asp Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly
 430 435 440
 45 Thr Leu Thr Glu Val Gly Ala Asp Pro Thr Glu Phe Ala Val Glu Pro Asp
 445 450 455
 Glu Phe His Ala Arg Leu Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met
 50 460 465 470 475
 Thr Thr Leu Ser Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg

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5 480 485 490
 Ile Ser Val Ile Ser Glu Val Ala Gly Asp Trp Glu Lys Ala Leu Asn Arg
 495 500 505 510
 10 Leu Arg Asp Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Ala Leu Leu Trp
 515 520 525
 Gln Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Tyr Tyr
 15 530 535 540
 Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Asn Trp Thr Asp Pro
 20 545 550 555 560
 Ala Pro Ala Phe Glu Glu Lys Leu Lys Ala Ala Val Asp Ala Val Phe Asp
 565 570 575
 Asn Pro Ala Val Gln Ala Glu Val Glu Ala Leu Val Glu Leu Leu Glu Pro
 25 580 585 590 595
 Tyr Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln Leu Thr Met Pro
 600 605 610
 30 Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp Asp Arg Ser Leu Thr
 615 620 625
 Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Asp Asp Arg Arg Ala Ala Leu
 35 630 635 640 645
 Glu Gln Leu Asp Ala Gly Asp Leu Pro Ala Ser Phe Thr Asp Glu Arg Thr
 650 655 660
 40 Lys Leu Leu Val Thr Ser Arg Ala Leu Arg Leu Arg Arg Asp Arg Pro Glu
 665 670 675 680
 Leu Phe Thr Gly Tyr Arg Pro Val Leu Ala Ser Gly Pro Ala Ala Gly His
 45 685 690 695
 Leu Leu Ala Phe Asp Arg Gly Thr Ala Ala Ala Pro Gly Ala Leu Thr Leu
 700 705 710
 50 Ala Thr Arg Leu Pro Tyr Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr
 715 720 725 730
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Ala Val Glu Leu Asn Thr Ala Met Lys Asp Glu Leu Thr Gly Ala Gly Phe

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Gly Pro Gly Ala Val Lys Ile Ala Asp Ile Phe Arg Ser Phe Pro Val Ala

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Leu Leu Val Pro Gln Thr Gly Gly Glu Ser

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34. The process as claimed in claim 28, wherein said DNA has a base sequence selected from the group consisting of those as shown in the following SEQ ID NOs:10 and 11:

SEQ ID NO:10:

CGTGCTCTAC TTCAACGCGC ACGACGGCGA CGTCGTGTTT AAGCTCCCGT CGGATGAATA 60

CGCCCCGGCC TGGGACGTCA TCATCGACAC CGCCGGCGCG GGTGCCGATT CCGAACCCGT 120

GCAGGCTGGC GGCAAACTCA CCGTGGCAGC GAAATCGCTC GTGGTGCTCC GTGCCCACAG 180

CGCCCCGGAG GAGGAACCGG ACCACTCGGT GGCCGCCTCC CTCGCAGCGC TGACGCAGAC 240

TGCGACCGCC GAAACCGCGG CGCTCACCGC CCCACCGTT CCGGAGCCGA GGAAGACCAA 300

GAAGGCAGCG CCGAAGCCGG AAGAGGAGGC TCCCGACGAG GCGGCGCCGA AGCCGGAAGA 360

GAAGGCTCCC GACGAGGCGG CGGCGAAGCC GGAAGAGGCT GCTTCCGACG AGGCGGCGGC 420

GAAGCCGGA GAGAAGGCTC CCGACGAGGC GGCGGCGAAG CCGGAAGAGG CTGCTTCCGA 480

CGAGGCGGCG GCGAAGCCCG CGGGGAAGGC AGCGGCCAAA ACGGCCGGCA GGCGAGCGCC 540

AGGCAAGCAG GGCGGGACGG GCTC 564

ATG AGG ACA CCC GCC TCG ACC TAC CGG CTG CAG ATC AGG CGG GGT TTC 612

Met Arg Thr Pro Ala Ser Thr Tyr Arg Leu Gln Ile Arg Arg Gly Phe

1

5

10

15

ACG CTG TTT GAT GCC GCC GAG ACC GTG CCC TAC CTG AAG TCA CTC GGG 660

Thr Leu Phe Asp Ala Ala Glu Thr Val Pro Tyr Leu Lys Ser Leu Gly

20

25

30

GTG GAC TGG ATC TAC CTG TCG CCC ATC CTG AAG GCA GAG AGC GGC TCC 708

Val Asp Trp Ile Tyr Leu Ser Pro Ile Leu Lys Ala Glu Ser Gly Ser

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40

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5 GAC CAC GGC TAT GAC GTC ACC GAT CCC GCC GTA GTG GAC CCG GAG CGC 756
 Asp His Gly Tyr Asp Val Thr Asp Pro Ala Val Val Asp Pro Glu Arg
 50 55 60
 10 GGC GGC CCT GAA GGG CTG GCC GCG GTG TCC AAG GCG GCC CGC GGT GCC 804
 Gly Gly Pro Glu Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Gly Ala
 65 70 75 80
 15 GGC ATG GGC GTG CTG ATC GAC ATC GTG CCG AAC CAC GTG GGC GTG GCG 852
 Gly Met Gly Val Leu Ile Asp Ile Val Pro Asn His Val Gly Val Ala
 85 90 95
 20 TCG CCG CCG CAG AAC CCG TGG TGG TGG TCG CTG CTC AAG GAA GGG CGC 900
 Ser Pro Pro Gln Asn Pro Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg
 100 105 110
 25 GGG TCG CCC TAC GCC GTG GCG TTC GAC GTC GAC TGG GAC CTG GCG GGG 948
 Gly Ser Pro Tyr Ala Val Ala Phe Asp Val Asp Trp Asp Leu Ala Gly
 115 120 125
 30 GGC CGC ATC CGG ATC CCC GTC CTG GGC AGC GAC GAC GAT CTG GAC CAG 996
 Gly Arg Ile Arg Ile Pro Val Leu Gly Ser Asp Asp Asp Leu Asp Gln
 130 135 140
 35 CTC GAA ATC AAG GAC GGC GAG CTG CGG TAC TAC GAC CAC CGC TTC CCG 1044
 Leu Glu Ile Lys Asp Gly Glu Leu Arg Tyr Tyr Asp His Arg Phe Pro
 145 150 155 160
 40 CTG GCC GAG GGC AGC TAC CGG GAC GGC GAC TCC CCG CAG GAC GTC CAC 1092
 Leu Ala Glu Gly Ser Tyr Arg Asp Gly Asp Ser Pro Gln Asp Val His
 165 170 175
 45 GGC CGG CAG CAC TAC GAA CTC ATC GGC TGG CGG CGC GCC GAC AAT GAA 1140
 Gly Arg Gln His Tyr Glu Leu Ile Gly Trp Arg Arg Ala Asp Asn Glu
 180 185 190
 50 CTG AAC TAC CGC CGG TTC TTC GCG GTG AAC ACG CTC GCC GGC ATC CGG 1188
 Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu Ala Gly Ile Arg

5 195 200 205
 GTG GAG GTG CCG CCG GTC TTC GAT GAA GCG CAC CAG GAG GTG GTG CGC 1236
 Val Glu Val Pro Pro Val Phe Asp Glu Ala His Gln Glu Val Val Arg
 10 210 215 220
 TGG TTC CGT GCG GGG CTC GCC GAC GGG CTG CGG ATC GAC CAC CCG GAC 1284
 Trp Phe Arg Ala Gly Leu Ala Asp Gly Leu Arg Ile Asp His Pro Asp
 15 225 230 235 240
 GGC CTG GCC GAT CCC GAG GGG TAT TTG AAG CGG CTC CGT GAG GTC ACC 1332
 Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val Thr
 20 245 250 255
 GGG GGC GCG TAC CTG CTC ATC GAA AAG ATC CTC GAG CCG GGC GAA CAG 1380
 Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln
 25 260 265 270
 TTG CCG GCC AGC TTC GAG TGC GAA GGC ACC ACC GGC TAC GAC GCC CTC 1428
 Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu
 30 275 280 285
 GCG GAT GTC GAC AGG GTC TTC GTG GAC CCG CGG GGA CAG GTG CCG CTG 1476
 Ala Asp Val Asp Arg Val Phe Val Asp Pro Arg Gly Gln Val Pro Leu
 35 290 295 300
 GAC CGT CTG GAC GCA CGG CTG CGC GGC GGT GCG CCG GCC GAC TAC GAG 1524
 Asp Arg Leu Asp Ala Arg Leu Arg Gly Gly Ala Pro Ala Asp Tyr Glu
 40 305 310 315 320
 GAC ATG ATC CGC GGG ACC AAG CGC CGG ATC ACC GAC GGC ATC CTG CAC 1572
 Asp Met Ile Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His
 45 325 330 335
 TCC GAG ATC CTG CGC CTT GCC AGG CTG GTG CCC GAG CAG ACC GGA ATT 1620
 Ser Glu Ile Leu Arg Leu Ala Arg Leu Val Pro Glu Gln Thr Gly Ile
 50 340 345 350
 CCC GGG GAG GCG GCC GCG GAT GCG ATC GCG GAG ATC ATC GCG GCC TTC 1668
 55

5 Pro Gly Glu Ala Ala Ala Asp Ala Ile Ala Glu Ile Ile Ala Ala Phe
 355 360 365
 CCG GTC TAC CGG TCC TAT CTT CCC GAG GGC GCG GAG ATC CTG AAG GAG 1716
 10 Pro Val Tyr Arg Ser Tyr Leu Pro Glu Gly Ala Glu Ile Leu Lys Glu
 370 375 380
 GCC TGC GAC CTC GCC GCG CGG AGG CGT CCG GAA CTG GGC CAG ACC GTC 1764
 15 Ala Cys Asp Leu Ala Ala Arg Arg Arg Pro Glu Leu Gly Gln Thr Val
 385 390 395 400
 CAG CTG CTG CAG CCG CTG CTG CTG GAT ACC GAC CTC GAG ATT TCC CGC 1812
 20 Gln Leu Leu Gln Pro Leu Leu Leu Asp Thr Asp Leu Glu Ile Ser Arg
 405 410 415
 AGG TTC CAG CAG ACC TCG GGA ATG GTC ATG GCC AAA GGC GTG GAG GAC 1860
 25 Arg Phe Gln Gln Thr Ser Gly Met Val Met Ala Lys Gly Val Glu Asp
 420 425 430
 ACC GCG TTC TTC CGC TAC AAC CGG CTG GGA ACG CTC ACC GAG GTG GGC 1908
 30 Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly Thr Leu Thr Glu Val Gly
 435 440 445
 GCC GAC CCC ACC GAG TTC TCG CTG GAA CCG GAG GAG TTT CAC GTC CGG 1956
 35 Ala Asp Pro Thr Glu Phe Ser Leu Glu Pro Glu Glu Phe His Val Arg
 450 455 460
 ATG GCC CGC CGG CAG GCC GAA CTC CCG CTC TCC ATG ACC ACC CTG AGC 2004
 40 Met Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met Thr Thr Leu Ser
 465 470 475 480
 ACG CAC GAC ACC AAG CGC AGC GAG GAC ACC CGG GCC CGG ATC TCG GTG 2052
 45 Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg Ile Ser Val
 485 490 495
 ATC GCC GAG GTC GCG CCT GAA TGG GAA AAG GCC CTG GAC AGG CTG AAC 2100
 50 Ile Ala Glu Val Ala Pro Glu Trp Glu Lys Ala Leu Asp Arg Leu Asn
 500 505 510

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5 ACC CTC GCT CCG CTG CCG GAC GGC CCG CTC TCC ACG CTG CTC TGG CAG 2148
 Thr Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Thr Leu Leu Trp Gln
 515 520 525
 10 GCG ATT GCG GGG GCA TGG CCG GCC AGC CGG GAA CGC CTT CAG TCC TAC 2196
 Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Ser Tyr
 530 535 540
 15 GCC CTG AAA GCG GCG CGC GAA GCC GGG AAC TCG ACC AGC TGG ACC GAT 2244
 Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Ser Trp Thr Asp
 545 550 555 560
 20 CCG GAC CCG GCA TTC GAG GAG GCA CTT TCC GCC GTC GTC GAC TCC GCC 2292
 Pro Asp Pro Ala Phe Glu Glu Ala Leu Ser Ala Val Val Asp Ser Ala
 565 570 575
 25 TTC GAC AAT CCG GAG GTG CGT GCG GAA CTT GAG GCC CTG GTG GGC CTC 2340
 Phe Asp Asn Pro Glu Val Arg Ala Glu Leu Glu Ala Leu Val Gly Leu
 580 585 590
 30 CTT GCG CCG CAC GGT GCG TCC AAC TCG CTC GCG GCA AAG CTT GTC CAG 2388
 Leu Ala Pro His Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln
 595 600 605
 35 CTG ACC ATG CCG GGC GTT CCG GAC GTG TAC CAG GGC ACC GAG TTC TGG 2436
 Leu Thr Met Pro Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp
 610 615 620
 40 GAC AGG TCG CTG ACC GAT CCG GAC AAC CGG CGC CCC TTC AGC TTC GCC 2484
 Asp Arg Ser Leu Thr Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Ala
 625 630 635 640
 45 GAA CGG ATT AGG GCC TTG GAC CAG TTG GAC GCC GGC CAC CGT CCG GAC 2532
 Glu Arg Ile Arg Ala Leu Asp Gln Leu Asp Ala Gly His Arg Pro Asp
 645 650 655
 50 TCC TTC CAG GAC GAG GCG GTC AAG CTG CTG GTC ACC TCG AGG GCG CTG 2580
 Ser Phe Gln Asp Glu Ala Val Lys Leu Leu Val Thr Ser Arg Ala Leu
 55

5 660 665 670
 CGG CTG CGG CGG AAC CGG CCC GAG CTC TTC ACC GGC TAC CGC CCC GTG 2628
 Arg Leu Arg Arg Asn Arg Pro Glu Leu Phe Thr Gly Tyr Arg Pro Val
 10 675 680 685
 CAT GCC AGG GGC CCC GCC GCC GGG CAC CTG GTG GCG TTC GAC CGC GGC 2676
 His Ala Arg Gly Pro Ala Ala Gly His Leu Val Ala Phe Asp Arg Gly
 15 690 695 700
 GCC GGG GGA GTG CTG GCG CTT GCC ACC CGG CTC CCC TAC GGG CTG GAA 2724
 Ala Gly Gly Val Leu Ala Leu Ala Thr Arg Leu Pro Tyr Gly Leu Glu
 20 705 710 715 720
 CAG TCG GGC GGC TGG CGG GAC ACC GCC GTC GAG CTT GAA GCC GCC ATG 2772
 Gln Ser Gly Gly Trp Arg Asp Thr Ala Val Glu Leu Glu Ala Ala Met
 25 725 730 735
 ACG GAC GAA CTG ACC GGC TCC ACT TTC GGG CCG GGA CCG GCG GCG CTG 2820
 Thr Asp Glu Leu Thr Gly Ser Thr Phe Gly Pro Gly Pro Ala Ala Leu
 30 740 745 750
 TCA GAA GTC TTC CGG GCC TAC CCG GTG GCC TTG TTG GTC CCC GCG ACA 2868
 Ser Glu Val Phe Arg Ala Tyr Pro Val Ala Leu Leu Val Pro Ala Thr
 35 755 760 765
 GGA GGC AAG TCA 2880
 Gly Gly Lys Ser
 40 770
 TGACGCAGCC CAACGATGCG GCCAAGCCGG TGCAGGGAGC GGGGCGCTTC GATATC 2936
 45
 50
 55

SEQ ID NO:11

5 GATCCGGACG GCAACCTCAT GTCCCCGGAG GACTGGGACA GCGGCTTCGG CCGTTCGGTG 60
GGCATGTTCC TCAACGGCGA CGGCATCCAG GGCCACGATG ACCGCGGCCG CCGCATCACG 120
GACGTGAACT TCCTGCTGTA CTTCAACGCC CACGACGGCG ACGTCGAGTT CACGCTGCCG 180
10 CCGGACGAAT ACGCCCCGGC CTGGGACGTC ATCATCGACA CCGCCGGTGA AGGGGCCGAC 240

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5 TCCAAGCCCCG CGGACGCCGG AACCATCCTG TCCGTTGCCG CCAAGTCGCT GGTGTGCTT 300
 CGCGCCCACA GCGCACC GGA GGAGAGCCT GACCATTCCG TGGCTGCTTC CCTGGCTGCA 360
 CTGACGCAGA CCGCCACCGC CGAGACGGCG GCGCTCACAG CTCCTGCCGT TCCCGAGCCG 420
 10 GCCAAGACGA AGAAGCCGGC CGCTGACCCG GTTGCTGAAC CGGCCGACCC GCCGGTTGCT 480
 GACCCGGCCG ACCCGGTTGC TGACCCGGTT GCTGACCCGG CGCCGGAACC GGCTGCGGAG 540
 CCTGCGAAAT CCGCAGCGGA ACCTGGTGCG GAGCCTGCGA AGGACCCGGA GGAGCAGCCG 600
 15 GCGGAAAAGC CGGCGCGCAA GCCTGCGGCA AAGCGCGGCG GCCACCTGAG GGCGGTCAAG 660
 CCCGCTGGGG AGGACGC 677
 ATG AGA ACG CCA GTC TCC ACG TAC AGG CTG CAG ATC AGG AAG GGA TTC 725
 20 Met Arg Thr Pro Val Ser Thr Tyr Arg Leu Gln Ile Arg Lys Gly Phe
 1 5 10 15
 ACA CTC TTC GAC GCG GCC AAA ACC GTT CCG TAC CTG CAC TCG CTC GGC 773
 25 Thr Leu Phe Asp Ala Ala Lys Thr Val Pro Tyr Leu His Ser Leu Gly
 20 25 30
 GTC GAC TGG GTC TAC CTT TCT CCG GTC CTG ACT GCC GAG CAG GGC TCC 821
 30 Val Asp Trp Val Tyr Leu Ser Pro Val Leu Thr Ala Glu Gln Gly Ser
 35 40 45
 GAC CAC GGG TAC GAC GTC ACC GAT CCC TCC GCC GTC GAC CCC GAA CGC 869
 35 Asp His Gly Tyr Asp Val Thr Asp Pro Ser Ala Val Asp Pro Glu Arg
 50 55 60
 GGC GGG CCG GAG GGC CTC GCG GCG GTT TCC AAG GCG GCC CGC GCC GCG 917
 40 Gly Gly Pro Glu Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Ala Ala
 65 70 75 80
 GGC ATG GGC GTG CTG ATC GAC ATC GTG CCC AAC CAC GTG GGC GTC GCG 965
 45 Gly Met Gly Val Leu Ile Asp Ile Val Pro Asn His Val Gly Val Ala
 85 90 95
 50 ACG CCG GCG CAG AAC CCC TGG TGG TGG TCG CTG CTC AAG GAG GGA CGC 1013
 Thr Pro Ala Gln Asn Pro Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg
 100 105 110

5 CAG TCC CGT TAC GCG GAG GCG TTC GAC GTC GAT TGG GAC CTC GCC GGG 1061
 Gln Ser Arg Tyr Ala Glu Ala Phe Asp Val Asp Trp Asp Leu Ala Gly
 115 120 125
 10 GGA CGC ATC CGG CTG CCG GTG CTC GGC AGC GAC GAT GAC CTC GAC CAG 1109
 Gly Arg Ile Arg Leu Pro Val Leu Gly Ser Asp Asp Asp Leu Asp Gln
 130 135 140
 15 CTC GAA ATC AGG GAC GGG GAG CTG CGG TAC TAC GAC CAC CGA TTC CCG 1157
 Leu Glu Ile Arg Asp Gly Glu Leu Arg Tyr Tyr Asp His Arg Phe Pro
 145 150 155 160
 20 CTC GCC GAG GGA ACC TAC GCC GAA GGC GAC GCC CCG CGG GAT GTC CAC 1205
 Leu Ala Glu Gly Thr Tyr Ala Glu Gly Asp Ala Pro Arg Asp Val His
 165 170 175
 25 GCC CGG CAG CAC TAC GAG CTC ATC GGC TGG CGC CGC GCG GAC AAC GAG 1253
 Ala Arg Gln His Tyr Glu Leu Ile Gly Trp Arg Arg Ala Asp Asn Glu
 180 185 190
 30 CTG AAC TAC CGC CGC TTT TTC GCG GTG AAC ACG CTC GCC GGC GTC CGC 1301
 Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu Ala Gly Val Arg
 195 200 205
 35 GTG GAA ATC CCC GCC GTC TTC GAC GAG GCA CAC CAG GAG GTG GTG CGC 1349
 Val Glu Ile Pro Ala Val Phe Asp Glu Ala His Gln Glu Val Val Arg
 210 215 220
 40 TGG TTC CGC GAG GAC CTT GCG GAC GGC CTG CGG ATC GAC CAC CCG GAC 1397
 Trp Phe Arg Glu Asp Leu Ala Asp Gly Leu Arg Ile Asp His Pro Asp
 225 230 235 240
 45 GGC CTC GCT GAC CCC GAG GGG TAC CTG AAG CGA CTC CGG GAA GTC ACC 1445
 Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val Thr
 245 250 255
 50 GGC GGC GCT TAC CTG CTG ATC GAA AAG ATC CTG GAG CCG GGG GAG CAG 1493
 Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln
 55

5 260 265 270
 CTG CCC GCC AGC TTC GAG TGT GAA GGC ACC ACA GGC TAC GAC GCC CTC. 1541
 Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu
 10 275 280 285
 GCC GAC GTC GAC CGG GTT CTC GTG GAC CCG CGC GGC CAG GAA CCG CTG 1589
 Ala Asp Val Asp Arg Val Leu Val Asp Pro Arg Gly Gln Glu Pro Leu
 15 290 295 300
 GAC CGG CTT GAC GCG TCC CTG CGT GGC GGC GAG CCC GCC GAC TAC CAG 1637
 Asp Arg Leu Asp Ala Ser Leu Arg Gly Gly Glu Pro Ala Asp Tyr Gln
 20 305 310 315 320
 GAC ATG ATC CGC GGA ACC AAG CGC CGG ATC ACC GAC GGT ATC CTG CAC 1685
 Asp Met Ile Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His
 25 325 330 335
 TCG GAG ATC CTG CGG CTG GCC CGG CTG GTT CCG GGC GAC GCC AAC GTT 1733
 Ser Glu Ile Leu Arg Leu Ala Arg Leu Val Pro Gly Asp Ala Asn Val
 30 340 345 350
 TCA ATC GAC GCC GGA GCC GAC GCT CTC GCC GAA ATC ATC GCC GCC TTC 1781
 Ser Ile Asp Ala Gly Ala Asp Ala Leu Ala Glu Ile Ile Ala Ala Phe
 35 355 360 365
 CCG GTC TAC CGC ACC TAC CTG CCG GAG GGC GCC GAG GTC CTG AAG GAG 1829
 Pro Val Tyr Arg Thr Tyr Leu Pro Glu Gly Ala Glu Val Leu Lys Glu
 40 370 375 380
 GCG TGC GAG CTT GCC GCG CGT AGG CGG CCG GAA CTC GAC CAG GCC ATC 1877
 Ala Cys Glu Leu Ala Ala Arg Arg Arg Pro Glu Leu Asp Gln Ala Ile
 45 385 390 395 400
 CAG GCT CTG CAG CCG CTG CTG CTG GAC ACG GAC CTC GAG CTT GCC CGG 1925
 Gln Ala Leu Gln Pro Leu Leu Leu Asp Thr Asp Leu Glu Leu Ala Arg
 50 405 410 415
 CGC TTC CAG CAG ACC TCG GGC ATG GTC ATG GCC AAG GGC GTG GAG GAC 1973
 55

5 Arg Phe Gln Gln Thr Ser Gly Met Val Met Ala Lys Gly Val Glu Asp
 420 425 430
 ACC GCG TTC TTC CGC TAC AAC CGC CTG GGC ACC CTC ACG GAA GTG GGC 2021
 10 Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly Thr Leu Thr Glu Val Gly
 435 440 445
 GCC GAC CCC ACC GAG TTC GCC GTG GAG CCG GAC GAG TTC CAC GCC CGG 2069
 15 Ala Asp Pro Thr Glu Phe Ala Val Glu Pro Asp Glu Phe His Ala Arg
 450 455 460
 CTG GCA CGC CGG CAG GCC GAG CTT CCG CTG TCC ATG ACG ACG CTG AGC 2117
 20 Leu Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met Thr Thr Leu Ser
 465 470 475 480
 ACG CAC GAC ACC AAG CGC AGC GAG GAC ACC CGA GCA AGG ATT TCG GTC 2165
 25 Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg Ile Ser Val
 485 490 495
 ATT TCC GAG GTT GCG GGT GAC TGG GAA AAG GCC TTG AAC CGG CTG CGC 2213
 30 Ile Ser Glu Val Ala Gly Asp Trp Glu Lys Ala Leu Asn Arg Leu Arg
 500 505 510
 GAC CTG GCC CCG CTG CCG GAC GGC CCG CTG TCC GCG CTG CTC TGG CAG 2261
 35 Asp Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Ala Leu Leu Trp Gln
 515 520 525
 GCC ATT GCC GGC GCC TGG CCC GCC AGC CGG GAA CGC CTG CAG TAC TAC 2309
 40 Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Tyr Tyr
 530 535 540
 GCG CTG AAG GCC GCG CGT GAA GCG GGG AAC TCG ACC AAC TGG ACC GAT 2357
 45 Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Asn Trp Thr Asp
 545 550 555 560
 CCG GCC CCC GCG TTC GAG GAG AAG CTG AAG GCC GCG GTC GAC GCC GTG 2405
 50 Pro Ala Pro Ala Phe Glu Glu Lys Leu Lys Ala Ala Val Asp Ala Val
 565 570 575
 55

5 TTC GAC AAT CCC GCC GTG CAG GCC GAG GTG GAA GCC CTC GTC GAG CTC 2453
 Phe Asp Asn Pro Ala Val Gln Ala Glu Val Glu Ala Leu Val Glu Leu
 580 585 590

10 CTG GAG CCG TAC GGA GCT TCG AAC TCC CTC GCC GCC AAG CTC GTG CAG 2501
 Leu Glu Pro Tyr Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln
 595 600 605

15 CTG ACC ATG CCC GGC GTC CCG GAC GTC TAC CAG GGC ACG GAG TTC TGG 2549
 Leu Thr Met Pro Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp
 610 615 620

20 GAC CGG TCG CTG ACG GAC CCG GAC AAC CGG CGG CCG TTC AGC TTC GAC 2597
 Asp Arg Ser Leu Thr Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Asp
 625 630 635 640

25 GAC CGC CGC GCC GCG CTG GAG CAG CTG GAT GCC GGC GAC CTT CCC GCG 2645
 Asp Arg Arg Ala Ala Leu Glu Gln Leu Asp Ala Gly Asp Leu Pro Ala
 645 650 655

30 TCA TTT ACC GAT GAG CGG ACG AAG CTG CTA GTG ACG TCG CGC GCG CTG 2693
 Ser Phe Thr Asp Glu Arg Thr Lys Leu Leu Val Thr Ser Arg Ala Leu
 660 665 670

35 CGG CTG CGC CGG GAC CGT CCG GAG CTG TTC ACG GGG TAC CGG CCG GTC 2741
 Arg Leu Arg Arg Asp Arg Pro Glu Leu Phe Thr Gly Tyr Arg Pro Val
 675 680 685

40 CTG GCC AGC GGG CCC GCC GCC GGG CAC CTG CTC GCG TTC GAC CGC GGC 2789
 Leu Ala Ser Gly Pro Ala Ala Gly His Leu Leu Ala Phe Asp Arg Gly
 690 695 700

45 ACC GCG GCG GCG CCG GGT GCA TTG ACC CTC GCC ACG CGG CTT CCC TAC 2837
 Thr Ala Ala Ala Pro Gly Ala Leu Thr Leu Ala Thr Arg Leu Pro Tyr
 705 710 715 720

50 GGG CTG GAA CAG TCG GGT GGA TGG CGG GAC ACC GCC GTC GAA CTT AAC 2885
 Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr Ala Val Glu Leu Asn

55

	725	730	735	
5	ACC GCC ATG AAA GAC GAA CTG ACC GGT GCC GGC TTC GGA CCG GGG GCA	2933		
	Thr Ala Met Lys Asp Glu Leu Thr Gly Ala Gly Phe Gly Pro Gly Ala			
	740	745	750	
10	GTG AAG ATC GCC GAC ATC TTC CGG TCG TTC CCC GTT GCG CTG CTG GTG	2981		
	Val Lys Ile Ala Asp Ile Phe Arg Ser Phe Pro Val Ala Leu Leu Val			
	755	760	765	
15	CCG CAG ACA GGA GGA GAG TCA	3002		
	Pro Gln Thr Gly Gly Glu Ser			
	770	775		
20	TGACGCACAC CTACCCGCGG GAAGCCGCGA AACCCGTCCT GGGCCCCGCA CGCTACGACG	3062		
	TCTGGGCGCC C	3073		

- 25 35. The process as claimed in 28, wherein said DNA is derived from a microorganism selected from the group consisting of the genera *Rhizobium*, *Arthrobacter*, *Brevibacterium*, *Flavobacterium*, *Micrococcus*, *Curto-*
bacterium, *Mycobacterium* and *Terrabacter*.
- 30 36. The process as claimed in claim 28, wherein said host is a microorganism of the species *Escherichia coli*.
37. The process as claimed in claim 28, wherein said self-replicable vector is plasmid vector Bluescript II SK(+).
- 35 38. The process as claimed in claim 28, wherein said transformant is inoculated into a liquid culture medium having a pH of 2-8, and cultured at a temperature of 25-65°C for 1-6 days.
39. The process as claimed in claim 28, wherein said recombinant enzyme in the culture is collected by one
40 or more methods selected from the group consisting of centrifugation, filtration, concentration, salting
out, dialysis, ion-exchange chromatography, gel filtration chromatography, hydrophobic chromatography,
affinity chromatography, gel electrophoresis and isoelectrophoresis.
40. A method to convert a reducing amylaceous saccharide, which contains a step of allowing the recombinant
45 enzyme of claim 25 to act on a reducing amylaceous saccharide having a degree of glucose polymerization
of 3 or higher to form a non-reducing saccharide having trehalose structure as an end unit from the amy-
laceous saccharide.
41. The method as claimed in claim 40, wherein said recombinant enzyme has the following physicochemical
properties:
50 (1) Molecular weight
About 76,000-87,000 daltons on sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PA-
GE); and
(2) Isoelectric point (pI)
About 3.6-4.6 on isoelectrophoresis.
- 55 42. The method as claimed in claim 40, wherein said recombinant enzyme has an amino acid sequence se-
lected from the group consisting of those as shown in the following SEQ ID NOs: 2 and 4 that initiate from
the N-terminal, and homologous amino acid sequences to these amino acid sequences:

SEQ ID NO:2

Met Arg Thr Pro Ala Ser Thr Tyr Arg Leu Gln Ile Arg Arg Gly Phe Thr
1 5 10 15
Leu Phe Asp Ala Ala Glu Thr Val Pro Tyr Leu Lys Ser Leu Gly Val Asp
20 25 30
Trp Ile Tyr Leu Ser Pro Ile Leu Lys Ala Glu Ser Gly Ser Asp His Gly
35 40 45 50

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5 Tyr Asp Val Thr Asp Pro Ala Val Val Asp Pro Glu Arg Gly Gly Pro Glu
 55 60 65
 Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Gly Ala Gly Met Gly Val Leu
 10 70 75 80 85
 Ile Asp Ile Val Pro Asn His Val Gly Val Ala Ser Pro Pro Gln Asn Pro
 90 95 100
 15 Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg Gly Ser Pro Tyr Ala Val Ala
 105 110 115
 Phe Asp Val Asp Trp Asp Leu Ala Gly Gly Arg Ile Arg Ile Pro Val Leu
 20 120 125 130 135
 Gly Ser Asp Asp Asp Leu Asp Gln Leu Glu Ile Lys Asp Gly Glu Leu Arg
 140 145 150
 25 Tyr Tyr Asp His Arg Phe Pro Leu Ala Glu Gly Ser Tyr Arg Asp Gly Asp
 155 160 165 170
 Ser Pro Gln Asp Val His Gly Arg Gln His Tyr Glu Leu Ile Gly Trp Arg
 30 175 180 185
 Arg Ala Asp Asn Glu Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu
 190 195 200
 35 Ala Gly Ile Arg Val Glu Val Pro Pro Val Phe Asp Glu Ala His Gln Glu
 205 210 215 220
 Val Val Arg Trp Phe Arg Ala Gly Leu Ala Asp Gly Leu Arg Ile Asp His
 40 225 230 235
 Pro Asp Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val
 240 245 250 255
 45 Thr Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln
 260 265 270
 Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu Ala
 50 275 280 285
 Asp Val Asp Arg Val Phe Val Asp Pro Arg Gly Gln Val Pro Leu Asp Arg

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5 290 295 300 305
 Leu Asp Ala Arg Leu Arg Gly Gly Ala Pro Ala Asp Tyr Glu Asp Met Ile
 310 315 320
 10 Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His Ser Glu Ile Leu
 325 330 335 340
 Arg Leu Ala Arg Leu Val Pro Glu Gln Thr Gly Ile Pro Gly Glu Ala Ala
 15 345 350 355
 Ala Asp Ala Ile Ala Glu Ile Ile Ala Ala Phe Pro Val Tyr Arg Ser Tyr
 360 365 370
 20 Leu Pro Glu Gly Ala Glu Ile Leu Lys Glu Ala Cys Asp Leu Ala Ala Arg
 375 380 385 390
 Arg Arg Pro Glu Leu Gly Gln Thr Val Gln Leu Leu Gln Pro Leu Leu Leu
 25 395 400 405
 Asp Thr Asp Leu Glu Ile Ser Arg Arg Phe Gln Gln Thr Ser Gly Met Val
 410 415 420 425
 30 Met Ala Lys Gly Val Glu Asp Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly
 430 435 440
 Thr Leu Thr Glu Val Gly Ala Asp Pro Thr Glu Phe Ser Leu Glu Pro Glu
 35 445 450 455
 Glu Phe His Val Arg Met Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met
 460 465 470 475
 40 Thr Thr Leu Ser Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg
 480 485 490
 Ile Ser Val Ile Ala Glu Val Ala Pro Glu Trp Glu Lys Ala Leu Asp Arg
 45 495 500 505 510
 Leu Asn Thr Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Thr Leu Leu Trp
 515 520 525
 50 Gln Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Ser Tyr
 530 535 540
 55

5 Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Ser Trp Thr Asp Pro
 545 550 555 560
 Asp Pro Ala Phe Glu Glu Ala Leu Ser Ala Val Val Asp Ser Ala Phe Asp
 10 565 570 575
 Asn Pro Glu Val Arg Ala Glu Leu Glu Ala Leu Val Gly Leu Leu Ala Pro
 580 585 590 595
 15 His Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln Leu Thr Met Pro
 600 605 610
 Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp Asp Arg Ser Leu Thr
 20 615 620 625
 Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Ala Glu Arg Ile Arg Ala Leu
 630 635 640 645
 25 Asp Gln Leu Asp Ala Gly His Arg Pro Asp Ser Phe Gln Asp Glu Ala Val
 650 655 660
 Lys Leu Leu Val Thr Ser Arg Ala Leu Arg Leu Arg Arg Asn Arg Pro Glu
 30 665 670 675 680
 Leu Phe Thr Gly Tyr Arg Pro Val His Ala Arg Gly Pro Ala Ala Gly His
 685 690 695
 35 Leu Val Ala Phe Asp Arg Gly Ala Gly Gly Val Leu Ala Leu Ala Thr Arg
 700 705 710
 Leu Pro Tyr Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr Ala Val Glu
 40 715 720 725 730
 Leu Glu Ala Ala Met Thr Asp Glu Leu Thr Gly Ser Thr Phe Gly Pro Gly
 735 740 745
 45 Pro Ala Ala Leu Ser Glu Val Phe Arg Ala Tyr Pro Val Ala Leu Leu Val
 750 755 760 765
 50 Pro Ala Thr Gly Gly Lys Ser
 770

5 SEQ ID NO:4
 Met Arg Thr Pro Val Ser Thr Tyr Arg Leu Gln Ile Arg Lys Gly Phe Thr
 1 5 10 15
 10 Leu Phe Asp Ala Ala Lys Thr Val Pro Tyr Leu His Ser Leu Gly Val Asp
 20 25 30
 Trp Val Tyr Leu Ser Pro Val Leu Thr Ala Glu Gln Gly Ser Asp His Gly
 15 35 40 45 50
 Tyr Asp Val Thr Asp Pro Ser Ala Val Asp Pro Glu Arg Gly Gly Pro Glu
 55 60 65
 20 Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Ala Ala Gly Met Gly Val Leu
 70 75 80 85
 Ile Asp Ile Val Pro Asn His Val Gly Val Ala Thr Pro Ala Gln Asn Pro
 25 90 95 100
 Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg Gln Ser Arg Tyr Ala Glu Ala
 105 110 115
 30 Phe Asp Val Asp Trp Asp Leu Ala Gly Gly Arg Ile Arg Leu Pro Val Leu
 120 125 130 135
 Gly Ser Asp Asp Asp Leu Asp Gln Leu Glu Ile Arg Asp Gly Glu Leu Arg
 35 140 145 150
 Tyr Tyr Asp His Arg Phe Pro Leu Ala Glu Gly Thr Tyr Ala Glu Gly Asp
 155 160 165 170
 40 Ala Pro Arg Asp Val His Ala Arg Gln His Tyr Glu Leu Ile Gly Trp Arg
 175 180 185
 Arg Ala Asp Asn Glu Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu
 45 190 195 200
 Ala Gly Val Arg Val Glu Ile Pro Ala Val Phe Asp Glu Ala His Gln Glu
 205 210 215 220
 50 Val Val Arg Trp Phe Arg Glu Asp Leu Ala Asp Gly Leu Arg Ile Asp His
 225 230 235

55

5 Pro Asp Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val
 240 245 250 255
 10 Thr Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln
 260 265 270
 Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu Ala
 275 280 285
 15 Asp Val Asp Arg Val Leu Val Asp Pro Arg Gly Gln Glu Pro Leu Asp Arg
 290 295 300 305
 20 Leu Asp Ala Ser Leu Arg Gly Gly Glu Pro Ala Asp Tyr Gln Asp Met Ile
 310 315 320
 Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His Ser Glu Ile Leu
 325 330 335 340
 25 Arg Leu Ala Arg Leu Val Pro Gly Asp Ala Asn Val Ser Ile Asp Ala Gly
 345 350 355
 30 Ala Asp Ala Leu Ala Glu Ile Ile Ala Ala Phe Pro Val Tyr Arg Thr Tyr
 360 365 370
 Leu Pro Glu Gly Ala Glu Val Leu Lys Glu Ala Cys Glu Leu Ala Ala Arg
 375 380 385 390
 35 Arg Arg Pro Glu Leu Asp Gln Ala Ile Gln Ala Leu Gln Pro Leu Leu Leu
 395 400 405
 40 Asp Thr Asp Leu Glu Leu Ala Arg Arg Phe Gln Gln Thr Ser Gly Met Val
 410 415 420 425
 Met Ala Lys Gly Val Glu Asp Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly
 430 435 440
 45 Thr Leu Thr Glu Val Gly Ala Asp Pro Thr Glu Phe Ala Val Glu Pro Asp
 445 450 455
 50 Glu Phe His Ala Arg Leu Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met
 460 465 470 475
 Thr Thr Leu Ser Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg

5 480 485 490
 Ile Ser Val Ile Ser Glu Val Ala Gly Asp Trp Glu Lys Ala Leu Asn Arg
 495 500 505 510
 10 Leu Arg Asp Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Ala Leu Leu Trp
 515 520 525
 15 Gln Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Tyr Tyr
 530 535 540
 Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Asn Trp Thr Asp Pro
 20 545 550 555 560
 Ala Pro Ala Phe Glu Glu Lys Leu Lys Ala Ala Val Asp Ala Val Phe Asp
 565 570 575
 25 Asn Pro Ala Val Gln Ala Glu Val Glu Ala Leu Val Glu Leu Leu Glu Pro
 580 585 590 595
 Tyr Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln Leu Thr Met Pro
 30 600 605 610
 Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp Asp Arg Ser Leu Thr
 615 620 625
 35 Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Asp Asp Arg Arg Ala Ala Leu
 630 635 640 645
 Glu Gln Leu Asp Ala Gly Asp Leu Pro Ala Ser Phe Thr Asp Glu Arg Thr
 40 650 655 660
 Lys Leu Leu Val Thr Ser Arg Ala Leu Arg Leu Arg Arg Asp Arg Pro Glu
 665 670 675 680
 45 Leu Phe Thr Gly Tyr Arg Pro Val Leu Ala Ser Gly Pro Ala Ala Gly His
 685 690 695
 Leu Leu Ala Phe Asp Arg Gly Thr Ala Ala Ala Pro Gly Ala Leu Thr Leu
 50 700 705 710
 Ala Thr Arg Leu Pro Tyr Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr
 715 720 725 730
 55

Ala Val Glu Leu Asn Thr Ala Met Lys Asp Glu Leu Thr Gly Ala Gly Phe

735

740

745

Gly Pro Gly Ala Val Lys Ile Ala Asp Ile Phe Arg Ser Phe Pro Val Ala

750

755

760

765

Leu Leu Val Pro Gln Thr Gly Gly Glu Ser

770

775

43. The method as claimed in claim 40, wherein said reducing amylaceous saccharide is a member selected from the group consisting of starch hydrolysate and amylaceous substance which has been treated with acid together with or without amylase.

44. The method as claimed in claim 40, wherein said reducing amylaceous saccharide is a member selected from the group consisting of maltotriose, maltotetraose, maltopentaose, maltohexaose, maltoheptaose and mixtures thereof.

45. The method as claimed in claim 40, wherein the reducing amylaceous saccharide is in a solution form with a concentration of 50 w/v % or lower, and the step is carried out at a temperature of 40-55°C and a pH of 5-10.

46. The method as claimed in claim 40, wherein said non-reducing saccharide is a member selected from the group of consisting of α -glucosyl trehalose, α -maltosyl trehalose, α -maltotriosyl trehalose, α -maltotetraosyl trehalose, α -maltopentaosyl trehalose, and mixtures thereof.

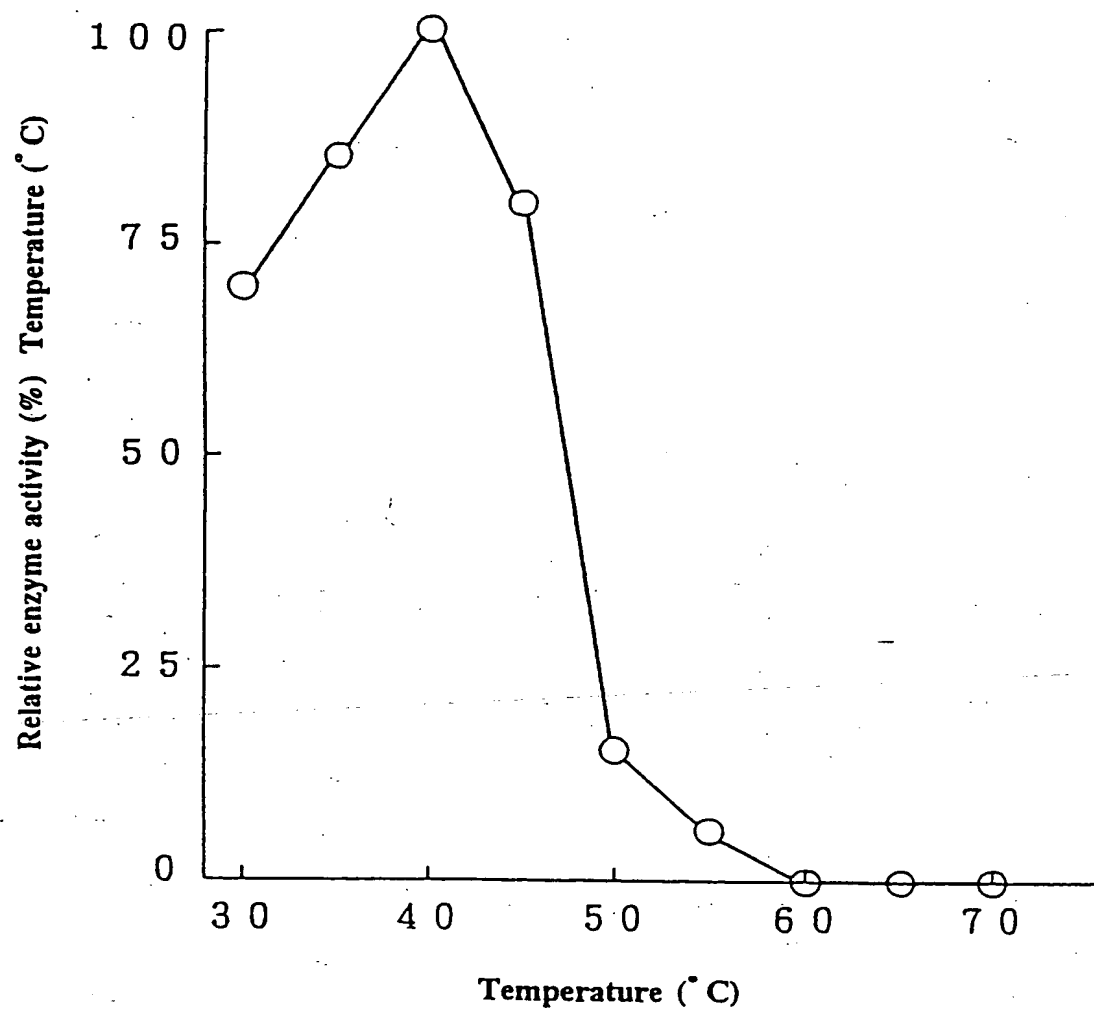


FIG. 1

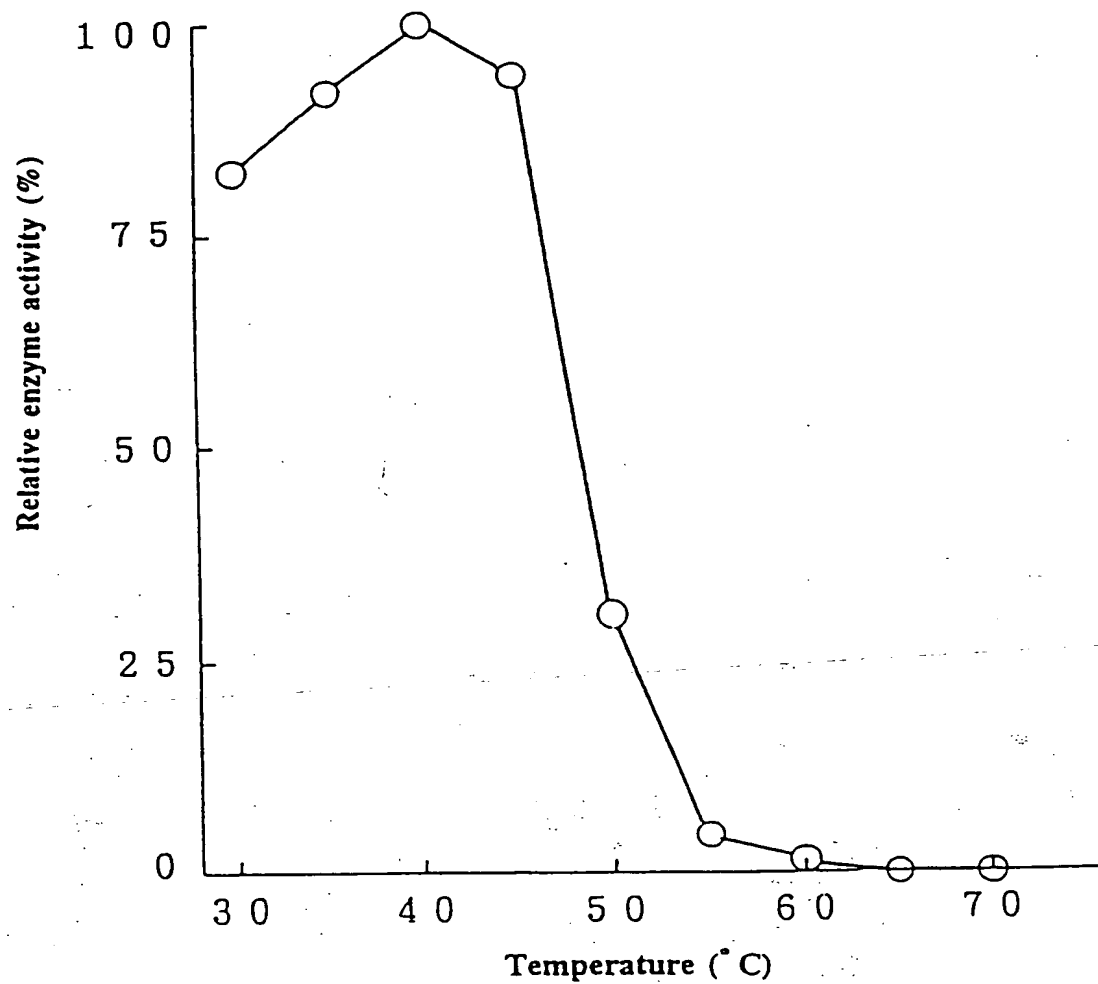


FIG. 2

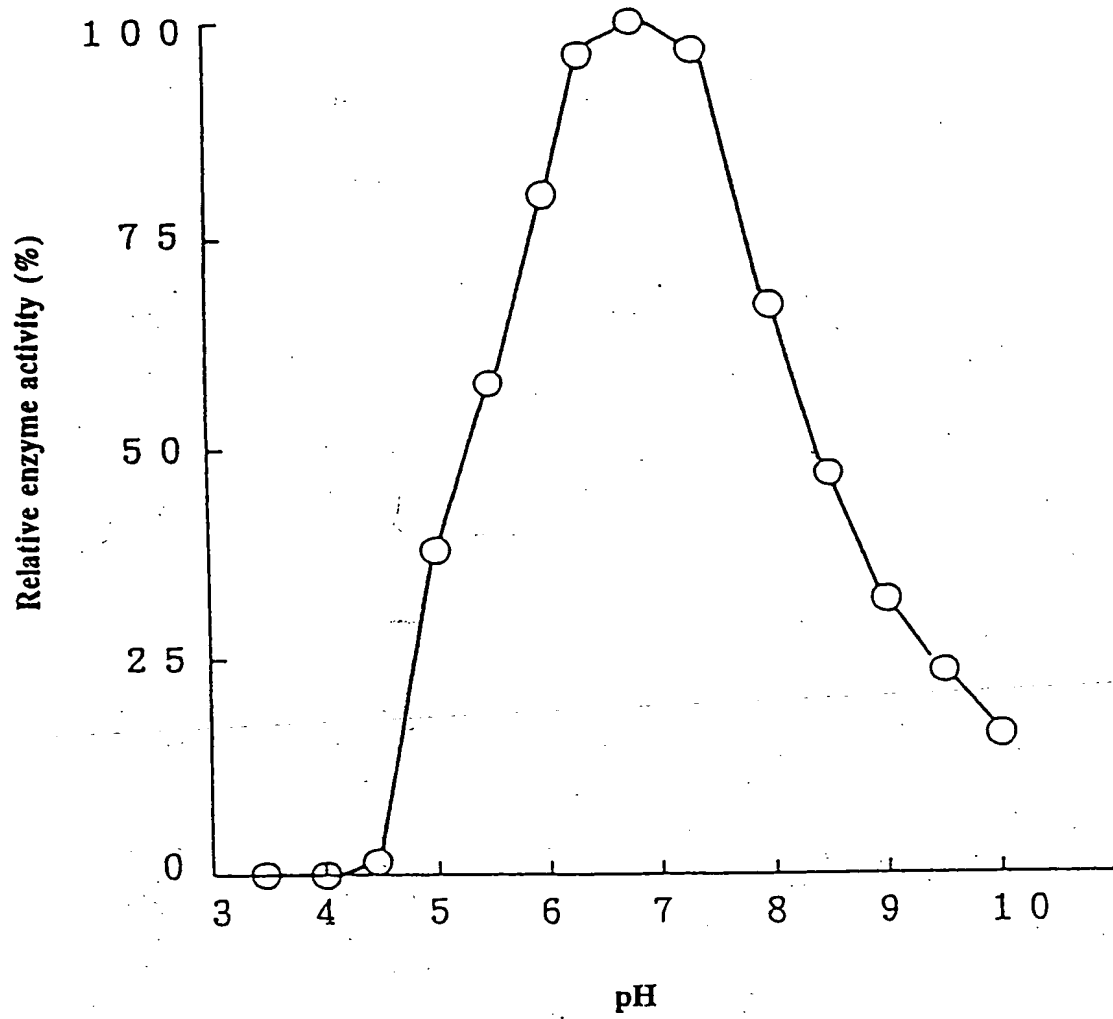


FIG. 3

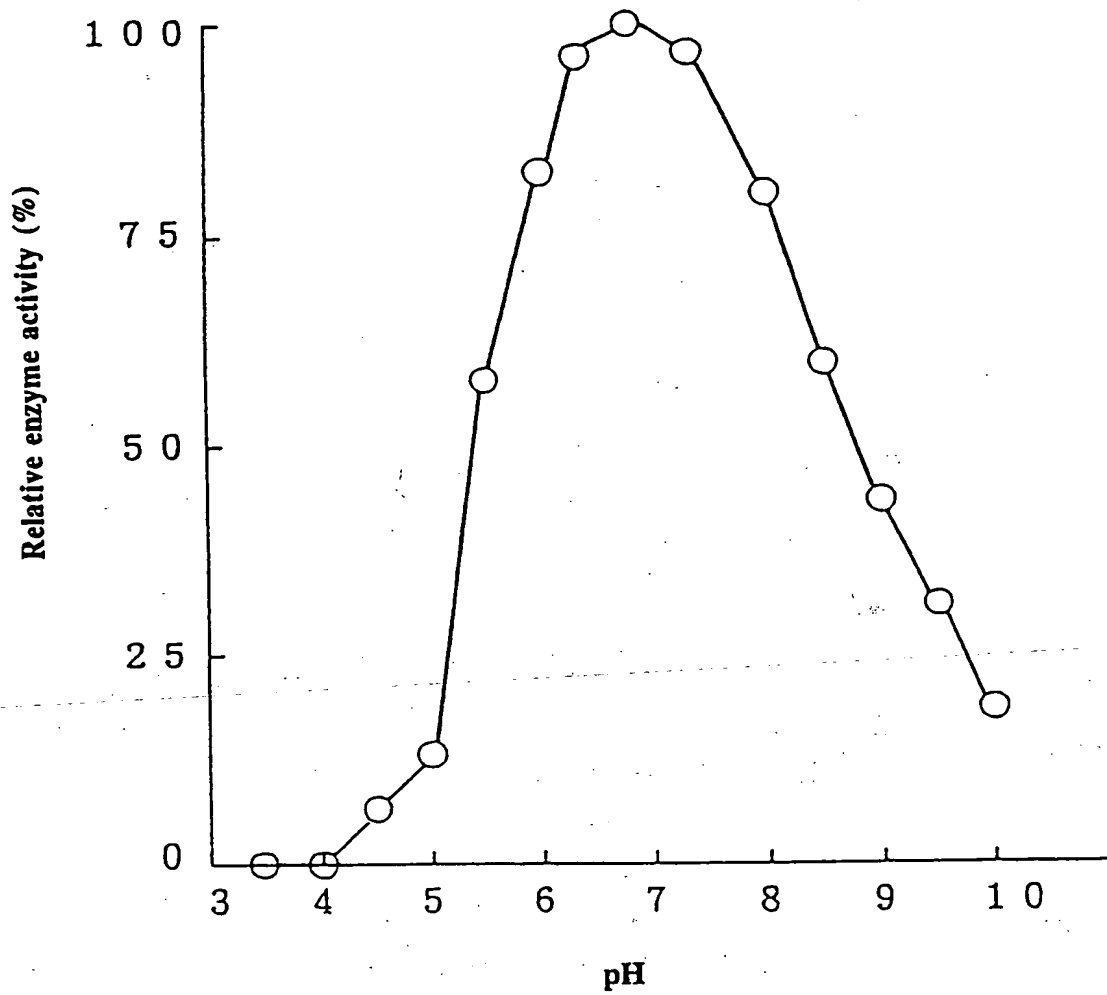


FIG. 4

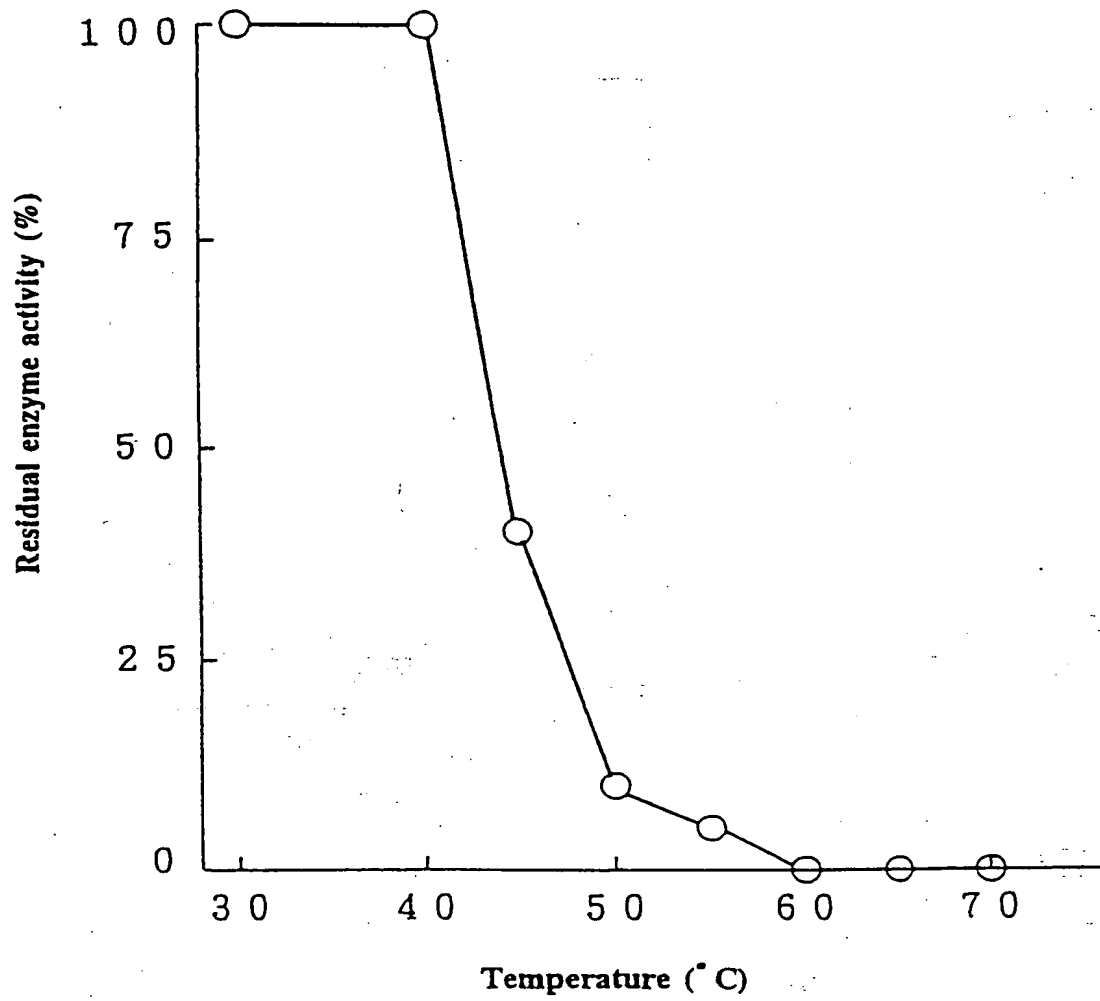


FIG. 5

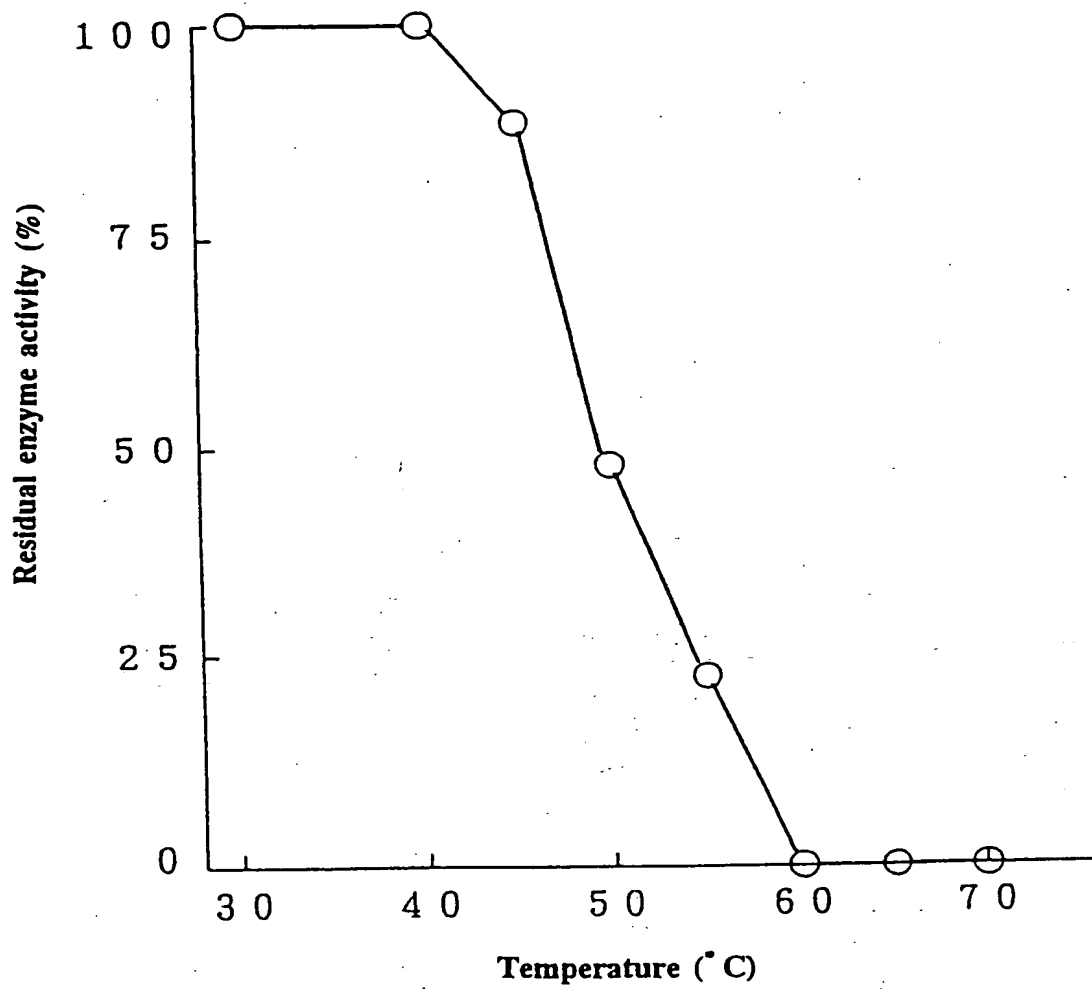


FIG. 6

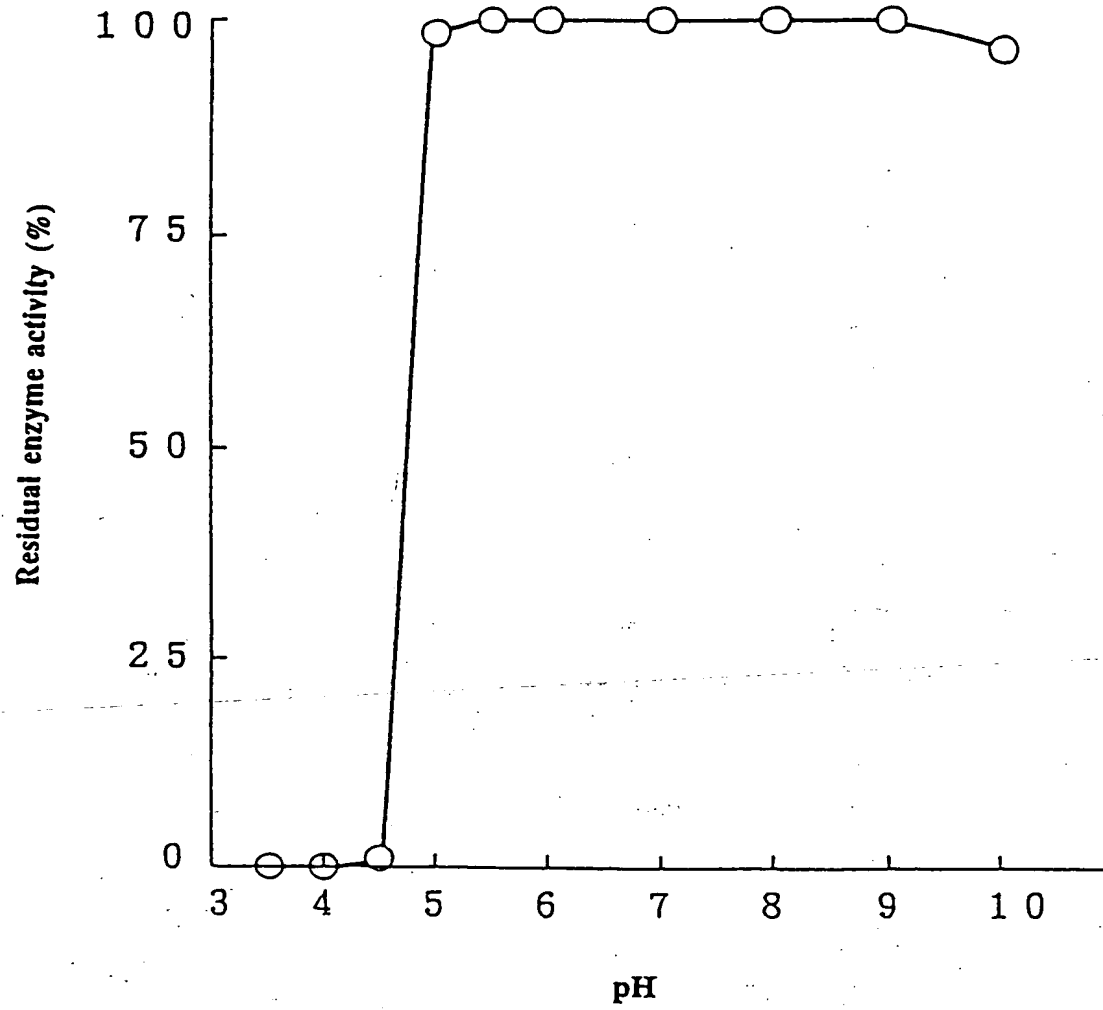


FIG. 7

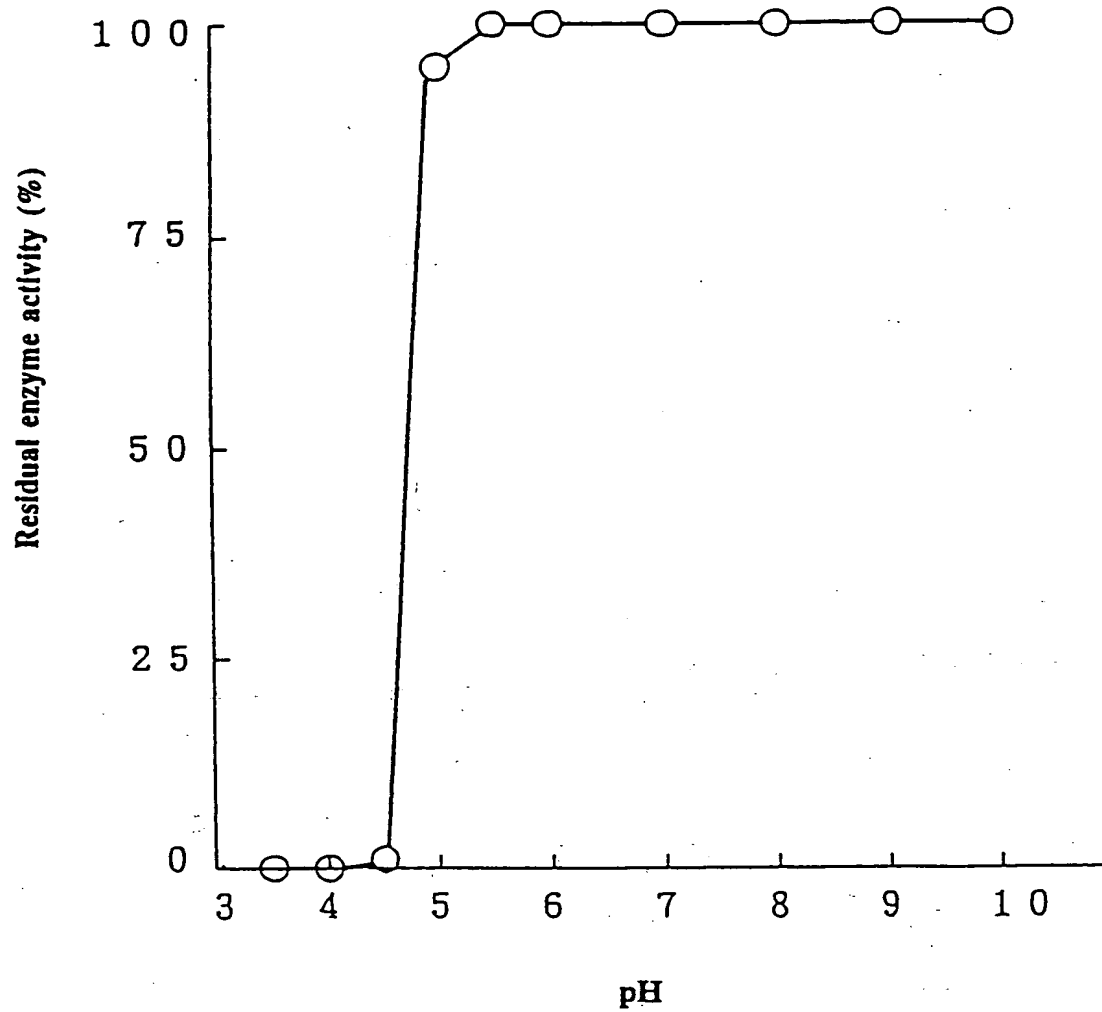


FIG. 8

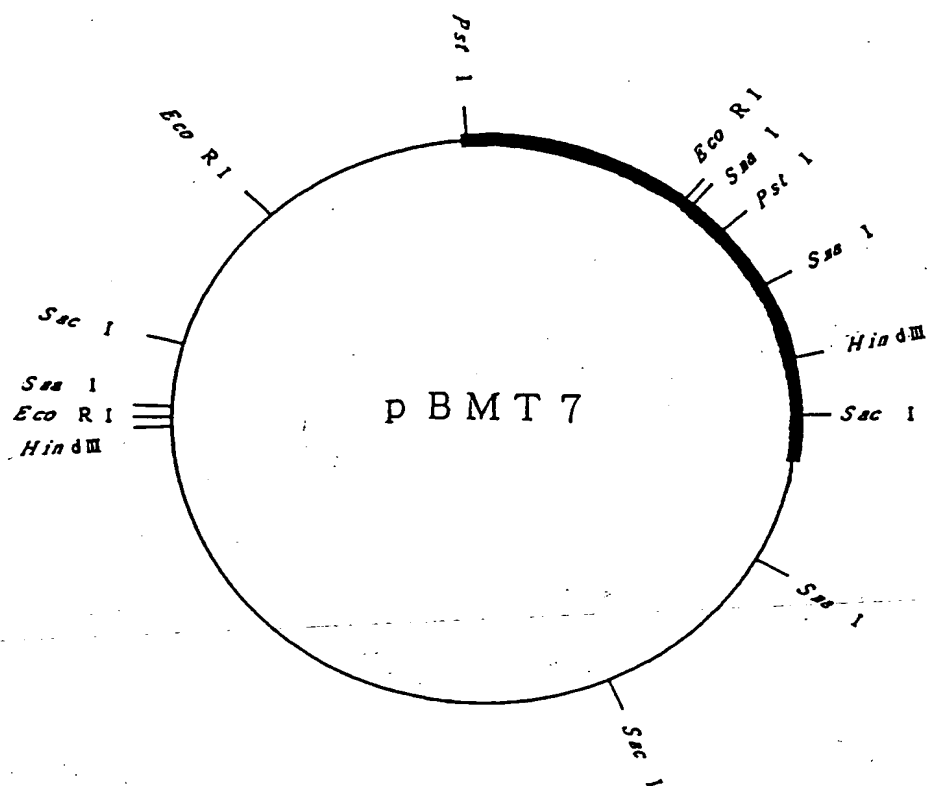


FIG. 9

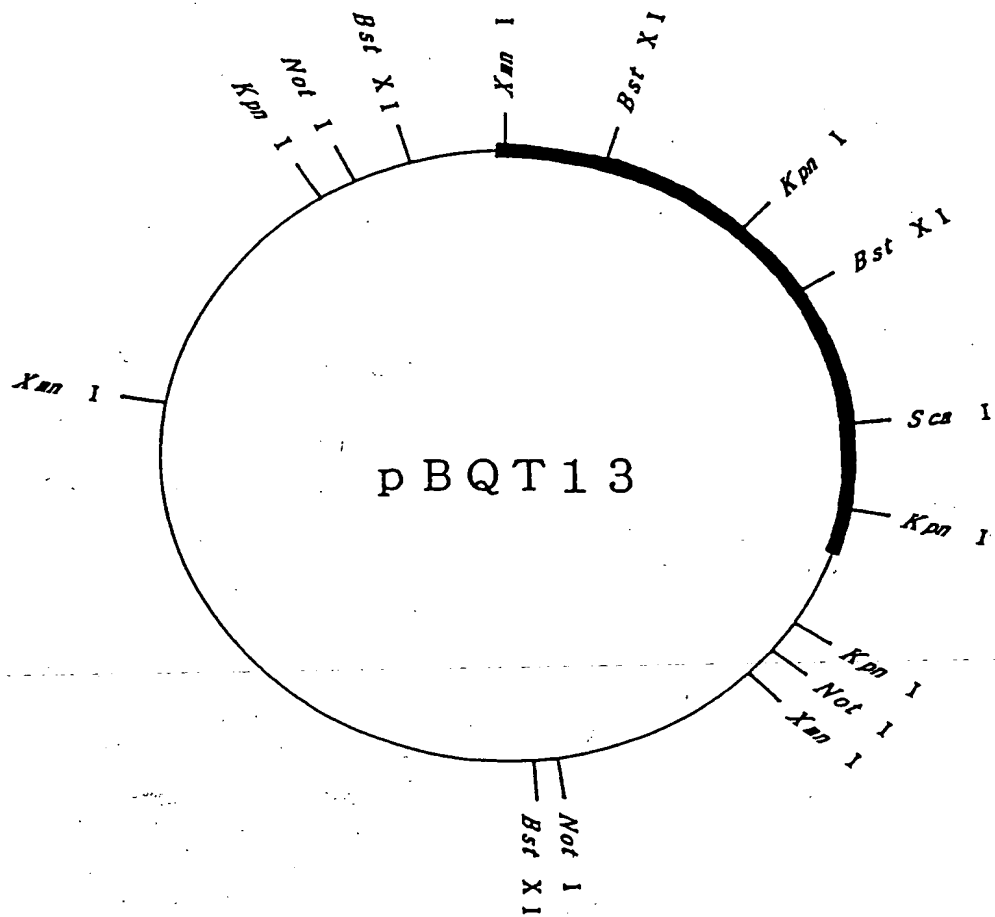


FIG. 10